



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 118660

TO: Nancy Vogel
Location: rem/2a65/2c70
Art Unit: 1636
Wednesday, April 07, 2004

Case Serial Number: 10/032393

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-B55
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Vogel,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
CM-1, Rm. 6-A-06
605-1155

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn. Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn.

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 7, 2004, 03:17:56 ; Search time 1681 Seconds

(without alignments)
1314.988 Million cell updates/sec

Title: US-10-032-393-36

Perfect score: 51

Sequence: 1 tcataaaaatttattgtc.....tttctgtataatagattca 51

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pac:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rod:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	60	6	A15398	A15398 Synthetic P
2	51	100.0	75	7	PT5PN25	M1602 Bacterioph
3	51	100.0	202	6	A10374	A10374 Nucleotide
4	51	100.0	202	6	A11246	A11246 vector pDS2
5	51	100.0	202	6	E00936	E00936 DNA sequenc
6	51	100.0	207	6	A10375	A10375 Nucleotide
7	51	100.0	247	6	A11242	A11242 vector pDS1
8	51	100.0	259	6	A10373	A10373 Nucleotide
9	51	100.0	1113	6	A02739	A02739 Artificial
10	51	100.0	1113	6	A14592	A14592 Synthetic:n
11	51	100.0	1221	6	A02296	A02296 Plasmid pDS
12	51	100.0	1221	6	A14593	A14593 Synthetic n
13	51	100.0	1866	6	A02227	A02227 Plasmid pDS
14	51	100.0	1866	6	A02295	A02295 Plasmid pDS
15	51	100.0	1866	6	A02740	A02740 Artificial
16	51	100.0	1866	6	A07053	A07053 Nucleotide
17	51	100.0	1866	6	A14594	A14594 Synthetic n
18	51	100.0	3403	6	A02228	A02228 Plasmid pDS
19	51	100.0	5767	6	AX035965	AX035965 Sequence
20	51	100.0	6000	12	U66308	U66308 Expression
21	51	100.0	6447	12	AF288421	AF288421 Synthetic
22	50	98.0	76	6	A11173	A11173 A T5 promot
23	46.4	91.0	524	12	SYNIFNGS	K01699 Human immu
24	46	90.2	73	6	A12013	A12013 oligonucleo
25	46	90.2	73	6	A12014	A12014 oligonucleo
26	42.8	83.9	83	6	A16630	A16630 Nucleotide
27	42.8	83.9	83	6	A16631	A16631 Nucleotide
28	39	76.5	68	6	E01976	E01976 DNA encodin
29	33.6	65.9	131	6	A50146	A50146 Sequence 3
30	33.4	65.5	125	6	A46760	A46760 Sequence 2
31	33.4	65.5	125	6	I89341	I89341 Sequence 2
32	33	64.7	116	6	A13088	A13088 Nucleotide
33	33	64.7	132	12	SYNADREIB1	M1661 Synthetic a
34	33	64.7	171	6	AR069843	AR069843 Sequence
35	33	64.7	173	6	A01257	A01257 Nucleotide
36	33	64.7	173	6	A01258	A01258 (reverse co
37	33	64.7	173	6	A13104	A13104 Nucleotide
38	33	64.7	173	6	A13105	A13105 Nucleotide
39	33	64.7	180	6	A01247	A01247 Nucleotide
40	33	64.7	180	6	A01248	A01248 (reverse co
41	33	64.7	180	6	A13094	A13094 Nucleotide
42	33	64.7	180	6	A13095	A13095 Nucleotide
43	33	64.7	319	12	ARIACI	X06035 Synthetic 1
44	33	64.7	396	6	A11819	A11819 Artificial
45	33	64.7	396	6	A11820	A11820 Artificial

ALIGNMENTS

RESULT 1
A15398
LOCUS A15398 60 bp DNA linear PAT 22-SEP-1995
DEFINITION Synthetic Phage T5 promoter P-N 25.
ACCESSION A15398
VERSION A15398.1 GI:1247805
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 60)
Bujard,H. and Le Grice,S.
New Gram positive expression control sequences

FEATURES
source
1..60
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51
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Db 1 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51

RESULT 2
PTSPN25
LOCUS PTSPN25 75 bp DNA linear PHG 28-APR-1993
DEFINITION Bacteriophage T5 promoter P-N 25.
ACCESSION M1602
VERSION M1602.1 GI:215985
KEYWORDS promoter region.
SOURCE Bacteriophage T5
ORGANISM Bacteriophage T5
VIRUSES: dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
T5-like viruses.
1 (bases 1 to 75)
Gentz,R. and Bujard,H.
Promoters recognized by Escherichia coli RNA polymerase selected by
function: highly efficient promoters from bacteriophage T5
JOURNAL J. Bacteriol. 164 (1), 70-77 (1985)
MEDLINE 8608105
PUBMED 3900050
COMMENT Original source text: Bacteriophage T5 DNA.
FEATURES
source
1..75
/organism="Bacteriophage T5"
/mol_type="genomic DNA"
/db_xref="taxon:10726"
56..>75
/note="bacteriophage T5 RNA"

ORIGIN Undetermined.

Query Match 100.0%; Score 51; DB 7; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51
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6 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 56

Db 6 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 56

RESULT 3
A10374
LOCUS A10374 202 bp DNA linear PAT 22-SEP-1993
DEFINITION Nucleotide sequence 21 from patent number EP0303925.
ACCESSION A10374
VERSION A10374.1 GI:490696
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 202)
Bujard,H. and Lanzer,M.
High repressible sequence for control of expression
Patent: EP 0303925-A 21 22-FEB-1989;
F. HOFFMANN-LA ROCHE AG
JOURNAL
TITLE
AUTHORS
REFERENCE
JOURNAL
FEATURES
source
1..202
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 202;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51
|||||
124 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 174

Db 124 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 174

RESULT 4
A11246
LOCUS A11246 202 bp DNA linear PAT 12-NOV-1993
DEFINITION vector pDS2/PN25x/0,t02+ XhoI/EcoRI fragment.
ACCESSION A11246
VERSION A11246.1 GI:491020
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 202)
Bujard,H. and Stueber,D.
New expression control sequence
Patent: EP 0186069-A 10 02-JUL-1986;
F. HOFFMANN-LA ROCHE AG
JOURNAL
TITLE
AUTHORS
REFERENCE
JOURNAL
FEATURES
source
1..202
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 202;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51
|||||
124 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 174

Db 124 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 174

RESULT 5
E00936
LOCUS E00936 202 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA sequence including promoter and operator hybrid 'P(N25X/)'.
ACCESSION E00936
VERSION E00936.1 GI:2169197
KEYWORDS JP 1986181386-A/1.
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
1 (bases 1 to 202)
Heruman,B. and Deletoritsuhi,S.
NOVEL DEVELOPMENT REGULATING ARRANGEMENT
Patent: JP 1986181386-A 1 14-AUG-1986;
F HOFFMANN LA ROCHE & CO AG
OS Escherichia coli
PN JP 1986181386-A/1
PD 14-AUG-1986
PF 16-DEC-1985 JP 1985282699
PR 17-DEC-1984 GB 84 8431818
PI HERUMAN BUYARUDO, DELETORITSUHI SUTERYUBAA
PC C12N15/00, C12N1/20, C12N9/10, C12P21/02, (C12N1/20, C12R1:19), PC
(C12N1/20,
PC C12R1:125), (C12N9/10, C12R1:19), (C12N9/10, C12R1:125), (C12P21/02, PC
C12R1:19),
PC (C12P21/02, C12R1:125);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;

CC anti-sense: No;
CC *source: strain=M15;
FH Key Location/Qualifiers
FH promoter 1..<173
FT /note='P25 promoter'
FT 174..>190
FT sig_peptide /note='lac operator'
FT
FEATURES
source
Location/Qualifiers
1..202
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 202;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 51
|||||
Db 124 TCATAAAAAATTATTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 174

RESULT 6
A10375 207 bp DNA linear PAT 22-SEP-1993
LOCUS Nucleotide sequence 22 from patent number EP0303925.
ACCESSION A10375
VERSION A10375.1 GI:490697
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 207)
AUTHORS Bujard,H. and Lanzer,M.
TITLE High repressible sequence for control of expression
JOURNAL Patent: EP 0303925-A 22 22-FEB-1989;
F. HOFFMANN-LA ROCHE AG
FEATURES
source
Location/Qualifiers
1..207
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 207;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 51
|||||
Db 124 TCATAAAAAATTATTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 174

RESULT 7
A11242 247 bp DNA linear PAT 12-NOV-1993
LOCUS vector pDS1/PN25 XhoI-fragment carrying promoter Pn25 is displayed.
DEFINITION A11242
ACCESSION A11242
VERSION A11242.1 GI:491016
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 247)
AUTHORS Bujard,H. and Stueber,D.
TITLE New expression control sequence
JOURNAL Patent: EP 0186069-A 6 02-JUL-1986;
F. HOFFMANN-LA ROCHE AG
FEATURES
source
Location/Qualifiers
1..247
/organism="synthetic construct"

/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 51
|||||
Db 124 TCATAAAAAATTATTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 174

RESULT 8

A10373 259 bp DNA linear PAT 22-SEP-1993
LOCUS Nucleotide sequence 20 from patent number EP0303925.
ACCESSION A10373
VERSION A10373.1 GI:490695
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
1 (bases 1 to 259)
AUTHORS Bujard,H. and Lanzer,M.
TITLE High repressible sequence for control of expression
JOURNAL Patent: EP 0303925-A 20 22-FEB-1989;
F. HOFFMANN-LA ROCHE AG
FEATURES
source
Location/Qualifiers
1..259
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 259;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 51
|||||
Db 130 TCATAAAAAATTATTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 180

RESULT 9

A02739 1113 bp DNA linear PAT 23-MAR-1993
LOCUS Artificial sequence of plasmid pDS5/RBSII, 3A+5A (XhoI/XbaI
DEFINITION fragment).
ACCESSION A02739
VERSION A02739.1 GI:345272
KEYWORDS chloramphenicol acetyltransferase.
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
1 (bases 1 to 1113)
AUTHORS Gentz,R., Le Grice,S., Mous,J. and Stueber,D.
TITLE ENV/GAG polypeptides
JOURNAL Patent: EP 0270114-A 5 08-JUN-1988;
F. HOFFMANN-LA ROCHE AG
FEATURES
source
Location/Qualifiers
1..1113
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

CDS

225..947
/codon_start=1
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/product="Chloramphenicol acetyltransferase"
/protein_id="CAA00265.1"
/db_xref="GI:345273"
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/translation="MRGSVDLQPSLAFFSGAKAKMEKKTGYTVDISQMRKEHFE"

AFQSVAGCTYNTQVQLDITAFLEKTVKKNKHKYPAFIHILARLNMNAHPEFRMAKDE
LVIWDSVHPCYTVFHEQETFFSLMSEYHDDFRQFLHYSQDVACYENLAYEPKGI
ENMFVFSANPMWVSFTSFDLVNANMNFAPVFTMGKYITQGDKVLMPLAIQVHHAACD
GFHVGRMLNELQCYCDEWQGA"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 1113;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTTGCTTTCAGAAAAATTTTCTGTATAATAGATTCA 51
125 TCATAAAAAATTATTTGCTTTCAGAAAAATTTTCTGTATAATAGATTCA 175

RESULT 10

A14592 1113 bp DNA circular PAT 21-FEB-1994

LOCUS Synthetic nucleotide sequence encoding chloramphenicol

DEFINITION acetyltransferase (plus 21 additional N-terminus amino acids).

ACCESSION A14592

VERSION A14592.1 GI:491830

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 1113)

AUTHORS Banwarth,W., Certz,U., Mous,J. and Stueber,D.

TITLE Polypeptides that elicit antibodies against AIDS virus

JOURNAL Patent: EP 0219106-A 5 22-APR-1987;

F. HOFFMANN-LA ROCHE AG

FEATURES Location/Qualifiers

source 1..1113

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

225..947

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/transl_table=11

/product="chloramphenicol acetyltransferase"

/protein_id="CAA01171.1"

/db_xref="GI:491831"

/db_xref="REMTREMBL:CAA01171"

/translation="MRGSVDLQPSLARFSGAKEMKKTIGYTVDISQMRKEHFE

AFQSVAGCTYNTQVQLDITAFLEKTVKKNKHKYPAFIHILARLNMNAHPEFRMAKDE

LVIWDSVHPCYTVFHEQETFFSLMSEYHDDFRQFLHYSQDVACYENLAYEPKGI

ENMFVFSANPMWVSFTSFDLVNANMNFAPVFTMGKYITQGDKVLMPLAIQVHHAACD

GFHVGRMLNELQCYCDEWQGA"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 1113;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTTGCTTTCAGAAAAATTTTCTGTATAATAGATTCA 51
125 TCATAAAAAATTATTTGCTTTCAGAAAAATTTTCTGTATAATAGATTCA 175

RESULT 11

A02296 1221 bp DNA linear PAT 18-MAY-1993

LOCUS Plasmid pDS6/RBSII,3A+5A DNA XhoI/XbaI-fragment.

ACCESSION A02296

VERSION A02296.1 GI:345259

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 1221)

AUTHORS Certz,U., Gentz,R. and Takacs,B.

TITLE Plasmidium falciparum merozoite antigen peptides

JOURNAL Patent: EP 0283829-A 17 28-SEP-1988;

F. HOFFMANN-LA ROCHE AG
Location/Qualifiers
1..1221

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 1221;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTTGCTTTCAGAAAAATTTTCTGTATAATAGATTCA 51
125 TCATAAAAAATTATTTGCTTTCAGAAAAATTTTCTGTATAATAGATTCA 175

RESULT 12

A14593 1221 bp DNA circular PAT 21-FEB-1994

LOCUS Synthetic nucleotide sequence of the XhoI/XbaI fragment of

DEFINITION pDS6/RBSII,3A+5A.

ACCESSION A14593

VERSION A14593.1 GI:491832

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 1221)

AUTHORS Banwarth,W., Certz,U., Mous,J. and Stueber,D.

TITLE Polypeptides that elicit antibodies against AIDS virus

JOURNAL Patent: EP 0219106-A 6 22-APR-1987;

F. HOFFMANN-LA ROCHE AG

FEATURES Location/Qualifiers

source 1..1221

/organism="synthetic construct"

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225..269

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/db_xref="GI:491833"

/db_xref="REMTREMBL:CAA01172"

/translation="MRGSVDLQPSLDSC"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTTGCTTTCAGAAAAATTTTCTGTATAATAGATTCA 51
125 TCATAAAAAATTATTTGCTTTCAGAAAAATTTTCTGTATAATAGATTCA 175

RESULT 13

A02227 1866 bp DNA linear PAT 29-APR-1996

LOCUS Plasmid pDS8/RBSII,SphI DNA for XhoI/XbaI fragment.

ACCESSION A02227

VERSION A02227.1 GI:490286

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 1866)

AUTHORS Doebeil,H., Eggimann,B., Gentz,R., Hochuli,E. and Stueber,D.

TITLE Fusion proteins and their purification

JOURNAL Patent: EP 0282042-A 1 14-SEP-1988;

FEATURES
source
F. HOFFMANN-LA ROCHE AG
Location/Qualifiers
1..1866

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 1866;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATATAAAATTATTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51
125 TCATATAAAATTATTGCTTTCAGGAAATTTTCTGTATATAGATTCA 175

RESULT 14
A02295 1866 bp DNA linear PAT 18-MAY-1993

LOCUS A02295 Plasmid pDS8/RBSII, Sphi DNA XhoI/XbaI-fragment.
DEFINITION A02295
ACCESSION A02295
VERSION A02295.1 GI:345258

KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 1866)
AUTHORS Certz,U., Gentz,R. and Takacs,B.
TITLE Plasmodium falciparum merozoite antigen peptides
JOURNAL Patent: EP 0283829-A 16 28-SEP-1988;
F. HOFFMANN-LA ROCHE AG

FEATURES

Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 1866;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATATAAAATTATTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51
Db 125 TCATATAAAATTATTGCTTTCAGGAAATTTTCTGTATATAGATTCA 175

RESULT 15

A02740 1866 bp DNA linear PAT 23-MAR-1993
LOCUS A02740 Artificial sequence of pDS8/RBSII plasmid (XhoI/XbaI fragment).
DEFINITION A02740
ACCESSION A02740
VERSION A02740.1 GI:345274

KEYWORDS

SOURCE dihydrofolate reductase.
ORGANISM synthetic construct
artificial sequences.

REFERENCE

AUTHORS Gentz,R., Le Grice,S., Mous,J. and Stueber,D.
TITLE ENV/GAG polypeptides
JOURNAL Patent: EP 0270114-A 6 08-JUN-1988;
F. HOFFMANN-LA ROCHE AG

FEATURES

Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

CDS

225..806
/codon_start=1
/transl_table=11
/product="dihydrofolate reductase"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 1866;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATATAAAATTATTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51
Db 125 TCATATAAAATTATTGCTTTCAGGAAATTTTCTGTATATAGATTCA 175

Search completed: April 7, 2004, 04:52:05
Job time : 1683 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2004, 02:08:25 ; Search time 244 Seconds
(without alignments)
887.943 Million cell updates/sec

Title: US-10-032-393-36
Perfect score: 51
Sequence: 1 tcataaaaaatttattgtct.....tttctgtataatagattca 51

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	51	6 ABK98620	Abk98620 Gram posi
2	51	100.0	51	8 ACD13871	Acid13871 Xyl-T5 pr
3	51	100.0	60	1 AAN70573	Aan70573 Coliphage
4	51	100.0	72	4 AAH74868	Aah74868 Oligonuc1
5	51	100.0	80	4 AAH74869	Aah74869 Oligonuc1
6	51	100.0	80	6 ABK98610	Abk98610 Gram posi
7	51	100.0	80	8 ACD13861	Acid13861 Xyl-T5 fu
8	51	100.0	94	6 ABK98589	Abk98589 XylO-T5 f
9	51	100.0	94	8 ACD13840	Acid13840 Oligonuc1
10	51	100.0	95	6 ABK98590	Abk98590 XylO-T5 f
11	51	100.0	95	8 ACD13841	Acid13841 Oligonuc1
12	51	100.0	200	1 AAN91066	Aan91066 Control s
13	51	100.0	202	1 AAN60262	Aan60262 Plasmid p
14	51	100.0	207	1 AAN91067	Aan91067 Control s
15	51	100.0	247	1 AAN60259	Aan60259 Coliphage
16	51	100.0	259	1 AAN91065	Aan91065 Control s
17	51	100.0	556	6 ABK98585	Abk98585 Gram posi
18	51	100.0	556	8 ACD13836	Acid13836 Xyl-T5 fu
19	51	100.0	1113	1 AAN80481	Aan80481 Xhol/Xbai
20	51	100.0	1221	1 AAN81153	Aan81153 XhoI/XbaI
21	51	100.0	1866	1 AAN80482	Aan80482 XhoI/XbaI
22	51	100.0	1866	1 AAN81356	Aan81356 Sequence

24	51	100.0	1866	1 AAN80955	Aan80955 XhoI-XbaI
25	51	100.0	3403	1 AAN80956	Aan80956 Plasmid p
26	51	100.0	5302	3 AAA98012	Aaa98012 Expressio
27	51	100.0	5767	3 AAA98014	Aaa98014 Expressio
28	51	100.0	6852	6 ABK98600	Abk98600 Vector px
29	51	100.0	6852	8 ACD13851	Acid13851 Xyl opera
30	50	98.0	1246	4 AAS50517	Aas50517 Staphyloc
31	46	90.2	77	1 AAN70113	Aan70113 Sequence
32	43	84.3	51	6 ABK98621	Abk98621 Gram posi
33	43	84.3	51	8 ACD13872	Acid13872 Xyl-T5 mu
34	43	84.3	80	6 ABK98611	Abk98611 Gram posi
35	43	84.3	80	8 ACD13862	Acid13862 Xyl-T5 mu
36	43	84.3	94	6 ABK98606	Abk98606 Xyl-T5 DD
37	43	84.3	94	8 ACD13857	Acid13857 Xyl-T5 mu
38	43	84.3	95	6 ABK98607	Abk98607 Xyl-T5 DD
39	43	84.3	6852	6 ABK98637	Abk98637 Vector px
40	43	84.3	6852	8 ACD13888	Acid13888 Xyl-T5 mu
41	42.8	83.9	83	1 AAN81195	Aan81195 Beta-lact
42	39.4	77.3	80	1 AAN80462	Aan80462 Expressio
43	39	76.5	68	1 AAN81260	Aan81260 Hybrid pr
44	36.4	71.4	41	1 AAN90998	Aan90998 Fragments
45	33.4	65.5	125	2 AAT04945	Aat04945 Fragment

ALIGNMENTS

RESULT 1	ABK98620	standard; DNA; 51 BP.
ID	ABK98620;	
XX		
AC	ABK98620;	
XX		
DT	07-AUG-2003 (revised)	
DT	21-OCT-2002 (first entry)	
XX		
DE	Gram positive bacteria Xyl-T5 fusion promoter #3.	
XX		
KW	ds; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;	
KW	P59; P1P2; PL; XylO; tetrO; trpO; malO; lambdaclO; cellular proliferation;	
KW	antibiotic.	
XX		
OS	Eubacteria.	
OS	Bacteriophage T5.	
OS	Synthetic.	
XX		
PN	WO200251982-A2.	
XX		
PD	04-JUL-2002.	
XX		
PF	21-DEC-2001; 2001WO-US050250.	
XX		
PR	27-DEC-2000; 2000US-0259434P.	
PR	06-SEP-2001; 2001US-00948993.	
XX		
PA	(ELIT-) ELITRA PHARM INC.	
XX		
PI	Haselbeck R, Wall D, Gross M;	
XX		
DR	WPI; 2002-575374/61.	
XX		
PT	Isolated nucleic acid comprises bacterial promoters modified to have	
PT	altered activity in at least one gram-positive organism, e.g. Bacillus	
PT	anthracis or Clostridium botulinum, useful for regulating gene expression	
PT	in bacteria.	
XX		
PS	Claim 2; Page 219; 246pp; English.	
XX		
CC	The invention relates to an isolated nucleic acid comprising a fusion	
CC	promoter comprising at least one promoter that is modified to have	
CC	altered activity in at least one gram-positive organism, or comprising	
CC	T5, CP25, P32, P59, P1P2 or PL linked to at least one operator consisting	

CC positioned so binding of a repressor to an operator represses
CC transcription from the fusion promoter. Also included are vectors and
CC host cells comprising the fusion promoters, a method of identifying genes
CC involved in cellular proliferation or required for proliferation of a
CC prokaryotic cell using the vector, a method of identifying compounds that
CC inhibit the proliferation of a prokaryotic cell using the vector, a
CC method of identifying a compound that reduces the activity or level of a
CC gene product required for proliferation of a cell using the vector, a
CC compound identified by the methods, a method of inhibiting the activity
CC or expression of a gene in an operon required for proliferation using the
CC vector, manufacturing an antibiotic comprising using the vector or cell
CC and identifying a nucleic acid with promoter activity in Enterococcus
CC faecalis. The fusion promoters are useful for regulating nucleic acid or
CC polypeptide expression, particularly for regulating gene expression in
CC bacteria and for identifying proliferation-regulated genes or molecules
CC with potential antibiotic activity. The modified promoters are also
CC useful for replacing endogenous promoters to create cells with specific
CC regulatable genes. The present sequence is a fusion promoter sequence of
CC the invention. (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 51 BP; 19 A; 5 C; 5 G; 22 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51
|||||
Db 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51

RESULT 2
ACD13871
ID ACD13871 standard; DNA; 51 BP.

XX ACD13871;
XX
DT 15-AUG-2003 (first entry)
XX
DE Xyl-T5 promoter sequence.

XX Promoter; ds; gram positive bacteria; Staphylococcus aureus;
KW Enterococcus faecalis; operator; xylO; teto; trpO; malO; lambda-clO;
XX cellular proliferation.

OS Bacteriophage T5.
OS Unidentified.

PN US2003027286-A1.

PD 06-FEB-2003.

PF 21-DEC-2001; 2001US-00032393.

PR 06-SEP-2000; 2000US-0230335P.
PR 27-DEC-2000; 2000US-0259434P.

PA (HASE/) HASEIBECK R.
PA (WALL/) WALL D.
PA (GROS/) GROSS M.

PI Haselbeck R, Wall D, Gross M;

DR WPI; 2003-479541/45.

PT New isolated nucleic acid comprising a fusion promoter having at least
PT one promoter that is modified to have altered activity in at least one
PT gram-positive organism, useful for regulating gene expression in
PT bacteria.

PS Claim 2; Page 80; 142pp; English.

XX The invention relates to an isolated nucleic acid comprising a fusion promoter having at least one promoter that is modified to have altered activity in at least one gram-positive organism, useful for regulating gene expression in bacteria.

CC promoter having at least one promoter that is modified to have altered
CC activity in at least one gram-positive organism (e.g. Staphylococcus
CC aureus or Enterococcus faecalis). The promoter is linked to at least one
CC operator selected from xylO, teto, trpO, malO and lambda-clO, which are
CC positioned such that the binding of at least one repressor to the
CC operator represses transcription from the fusion promoter. Also included
CC are a vector comprising the isolated nucleic acid, a host cell comprising
CC the nucleic acid. The fusion promoter is useful for identifying genes
CC involved in cellular proliferation, identifying a compound that reduces
CC the activity or level of a gene product required for proliferation of a
CC cell, inhibiting the activity or expression of a gene in an operon
CC required for proliferation, manufacturing an antibiotic, identifying a
CC gene that is required for proliferation of a prokaryotic cell,
CC identifying a compound that inhibits the proliferation of a prokaryotic
CC cell and regulating gene expression in bacteria. The present sequence is
CC a bacterial promoter suitable for inclusion in a fusion promoter of the
CC invention
XX
SQ Sequence 51 BP; 19 A; 5 C; 5 G; 22 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51
|||||
Db 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51

RESULT 3
AAN70573
ID AAN70573 standard; DNA; 60 BP.

XX AAN70573;

DT 25-MAR-2003 (revised)
DT 11-MAR-1991 (first entry)

DE Coliphage T5 promoter of Bacillus subtilis expression vector.

KW Expression vector; dihydrofolate reductase; IL-2; insulin; HTLV-III; tPA;
KW human renin; ds.

OS Coliphage T5.

XX Key Location/Qualifiers
FH -35_signal 16..21
FT /*tag= a
FT -10_signal 39..44
FT /*tag= b

PN BP207459-A.

PD 07-JAN-1987.

PF 27-JUN-1986; 86EP-00108774.

PR 05-JUL-1985; 85GB-00017071.

PA (HOFF) HOFFMANN-LA ROCHE AG.

PI Bujard H, Legrice S;

DR WPI; 1987-001183/01.

PT New gram positive expression control DNA sequences - useful for potent
PT and versatile gene expression of prokaryotic or eukaryotic proteins in
PT bacillus subtilis etc.

PS Disclosure; Table I; 53pp; English.

XX The gene fragment may be incorporated into a novel expression vector, for
XX the expression of a protein in a prokaryotic or eukaryotic host cell.

CC *Bacillus subtilis*. Proteins which may be encoded include: dihydrofolate
CC reductase; chloramphenicol acetyltransferase; malaria surface antigens;
CC IL-2; interferons; insulin; tPA; human renin and HTLV-III. (Updated on 25
CC -MAR-2003 to correct PI field.)
XX
SQ Sequence 60 BP; 23 A; 5 C; 6 G; 26 T; 0 U; 0 Other;

Query Match	100.0%;	Score 51;	DB 1;	Length 60;
Best Local Similarity	100.0%;	Pred. No. 2.1e-05;		
Matches 51; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATATAGATTCA 51

Db 1 TCATATAAAATTTATTTGCTTCAGGAAATTTTCTGTATATAGATTCA 51

RESULT 4

ID AAH74868 standard; DNA; 72 BP.

AC AAH74868;

DT 29-OCT-2001 (first entry)

DE Oligonucleotide used to create T5 promoter.

KW Recombinase; genetic engineering; monogenic disorder; ADA deficiency;
KW cystic fibrosis; familial-hypercholesterolaemia; haemophilia;
KW chronic granulomatous disease; Duchenne's muscular dystrophy;
KW Fanconi's disease; anemia; sickle-cell anemia; Gaucher's disease;
KW Hunter's syndrome; X-linked severe combined immunodeficiency; SCID;
KW infectious disease; acquired disorder; tumour; cancer; TS promoter; ss
XX
OS Synthetic.

PN WO200161049-A1.

PD 23-AUG-2001.

Pf 16-FEB-2001; 2001WO-US005269.

PR 18-FEB-2000; 2000US-0183759P.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Calos MP, Scilimenti CR;

DR WPI; 2001-522610/57.

PT Identifying altered recombinase, involves hybridizing recombination sites in cells having specific coding sequence, transformed with altered recombinase gene, and isolating cells having product of the sequence.

PS Disclosure; Page 59; 101pp; English.

The specification describes a method for identifying altered recombinases. The method comprises transforming cells with a first plasmid comprising two recombination sites and a coding sequence of interest, and a second plasmid encoding an altered recombinase; allowing recombination of the two recombination sites using the altered recombinase; screening and isolating transformed cells comprising the product of the sequence of interest; and identifying the altered recombinase. The altered recombinase is useful for site-specifically integrating a polynucleotide sequence of interest in a genome of a cell. It is also useful in genetic engineering of chromosomes of higher cells, and for the generation of transgenic cells, tissues, plants and animals. The altered recombinase is useful for treating monogenic disorders, e.g. ADA deficiency, cystic fibrosis, familial hypercholesterolaemia, anemia, chronic granulomatous disease, Duchenne's muscular dystrophy, haemophilia, Fanconi's disease, sickle-cell anemia, Gaucher's disease, Hunter's syndrome and X-linked severe combined immunodeficiency (SCID), infectious diseases including viral and bacterial infections, acquired disorders including solid tumours and haematological cancers such as

CC leukaemias and lymphomas, and other cancers. Oligonucleotides AAH74868-69
CC were used to create the T5 promoter, which was used to construct a
CC plasmid for use in the course of the invention
xx
SQ Sequence 72 BP; 27 A; 6 C; 11 G; 28 T; 0 U; 0 Other;

Query Match	100.0%;	Score 51;	DB 4;	Length 72;
Best Local Similarity	100.0%;	Pred. No. 2.1e-05;		
Matches 51; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 TCATAAAAAATTATTTGCTTTCAGGAAAATTTTCTGTATATAGATTCA 51
2 TCATAAAAAATTATTTGCTTTCAGGAAAATTTTCTGTATATAGATTCA 52
Db

RESULT 5

ID AAH74869 standard; DNA; 80 BP.

AC AAH74869;

DT 29-OCT-2001 (first entry)

DE Oligonucleotide used to create T5 promoter.

KW Recombinase; genetic engineering; monogenic disorder; ADA deficiency;
KW cystic fibrosis; familial-hypercholesterolaemia; haemophilia;
KW chronic granulomatous disease; Duchenne's muscular dystrophy;
KW Fanconi's disease; sickle-cell anemia; Gaucher's disease;
KW Hunter's syndrome; X-linked severe combined immunodeficiency; SCID;
KW infectious disease; acquired disorder; tumour; cancer; TS promoter; ss.
XX
OS Synthetic.

PN WO200161049-A1.

PD 23-AUG-2001.

PF 16-FEB-2001; 2001WO-US0005269.

PR 18-FEB-2000; 2000US-0183759P.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Calos MP, ScIimenti CR;

DR WPI; 2001-522610/57.

PT Identifying altered recombinase, involves hybridizing recombination sites
PT in cells having specific coding sequence, transformed with altered
PT recombinase gene, and isolating cells having product of the sequence.

PS Disclosure; Page 59; 101pp; English.

CC The specification describes a method for identifying altered
CC recombinases. The method comprises transforming cells with a first
CC plasmid comprising two recombination sites and a coding sequence of
CC interest, and a second plasmid encoding an altered recombinase; allowing
CC recombination of the two recombination sites using the altered
CC recombinase; screening and isolating transformed cells comprising the
CC product of the sequence of interest; and identifying the altered
CC recombinase. The altered recombinase is useful for site-specifically
CC integrating a polynucleotide sequence of interest in a genome of a cell.
CC It is also useful in genetic engineering of chromosomes of higher cells,
CC and for the generation of transgenic cells, tissues, plants and animals.
CC The altered recombinase is useful for treating monogenic disorders, e.g.
CC ADA deficiency, cystic fibrosis, familial-hypercholesterolaemia, anaemia,
CC chronic granulomatous disease, Duchenne's muscular dystrophy,
CC haemophilia, Fanconi's disease, sickle-cell anaemia, Gaucher's disease,
CC Hunter's syndrome and X-linked severe combined immunodeficiency (SCID),
CC infectious diseases including viral and bacterial infections, acquired
CC disorders including solid tumours and haematopoietic cancers, such as
CC leukaemias and lymphomas and other cancers. Oligonucleotides AAH74868-63

CC were used to create the T5 promoter, which was used to construct a
CC plasmid for use in the course of the invention
XX
SQ Sequence 80 BP; 29 A; 14 C; 9 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 4; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51
|||||
Db 75 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATATAGATTCA 25

RESULT 6
ABK98610
ID ABK98610 standard; DNA; 80 BP.
XX
AC ABK98610;

DT 07-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)

DE Gram positive bacteria Xyl-T5 fusion promoter #2.

XX
KM ds; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;
KW P59; P1P2; PL; xylO; teto; trpO; malO; lambdaclO; cellular proliferation;
antibiotic.

XX Eubacteria.
OS Bacteriophage T5.
OS Synthetic.

XX WO200251982-A2.

XX 04-JUL-2002.

PF 21-DEC-2001; 2001WO-US050250.

XX 27-DEC-2000; 2000US-0259434P.

PR 06-SEP-2001; 2001US-00948993.

XX (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Wall D, Gross M;

DR WPI; 2002-575374/61.

PT Isolated nucleic acid comprises bacterial promoters modified to have
PT altered activity in at least one gram-positive organism, e.g. Bacillus
PT anthracis or Clostridium botulinum, useful for regulating gene expression
in bacteria.

PS Claim 24; Page 217; 246pp; English.

XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter comprising at least one promoter that is modified to have
CC altered activity in at least one gram-positive organism, or comprising
CC T5, CP25, P32, P59, P1P2 or PL linked to at least one operator consisting
CC of xylO, teto, trpO, malO or lambdaclO, where at least one operator is
CC positioned so binding of a repressor to an operator represses
CC transcription from the fusion promoter. Also included are vectors and
CC host cells comprising the fusion promoters, a method of identifying genes
CC involved in cellular proliferation or required for proliferation of a
CC prokaryotic cell using the vector, a method of identifying compounds that
CC inhibit the proliferation of a prokaryotic cell using the vector, a
CC method of identifying a compound that reduces the activity or level of a
CC gene product required for proliferation of a cell using the vector, a
CC compound identified by the methods, a method of inhibiting the activity
CC or expression of a gene in an operon required for proliferation using the
CC vector, manufacturing an antibiotic comprising using the vector or cell
CC and identifying a nucleic acid with promoter activity in Enterococcus
CC faecalis. The fusion promoters are useful for regulating nucleic acid or

CC polypeptide expression, particularly for regulating gene expression in
CC bacteria and for identifying proliferation-required genes or molecules
CC with potential antibiotic activity. The modified promoters are also
CC useful for replacing endogenous promoters to create cells with specific
CC regulatable genes. The present sequence is a fusion promoter sequence of
CC the invention. (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 80 BP; 29 A; 8 C; 8 G; 35 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51
|||||
Db 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51

RESULT 7
ACD13861
ID ACD13861 standard; DNA; 80 BP.
XX
AC ACD13861;

DT 15-AUG-2003 (first entry)

DE Xyl-T5 fusion promoter #1.

XX
KM Promoter; ds; gram positive bacteria; Staphylococcus aureus;
KW Enterococcus faecalis; operator; xylO; teto; trpO; malO; lambda-clO;
cellular proliferation.

XX Bacteriophage T5.
OS Unidentified.

XX US2003027286-A1.

XX 06-FEB-2003.

PF 21-DEC-2001; 2001US-00032393.

XX 06-SEP-2000; 2000US-0230335P.

PR 27-DEC-2000; 2000US-0259434P.

XX (HASE/) HASELBECK R.

PA (WALL/) WALL D.
PA (GROS/) GROSS M.

PI Haselbeck R, Wall D, Gross M;

DR WPI; 2003-479541/45.

PT New isolated nucleic acid comprising a fusion promoter having at least
PT one promoter that is modified to have altered activity in at least one
PT gram-positive organism, useful for regulating gene expression in
bacteria.

PS Claim 24; Page 78; 142pp; English.

XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter having at least one promoter that is modified to have altered
CC activity in at least one gram-positive organism (e.g. Staphylococcus
CC aureus or Enterococcus faecalis). The promoter is linked to at least one
CC operator selected from xylO, teto, trpO, malO and lambda-clO, which are
CC positioned such that the binding of at least one repressor to the
CC operator represses transcription from the fusion promoter. Also included
CC are a vector comprising the isolated nucleic acid, a host cell comprising
CC the nucleic acid. The fusion promoter is useful for identifying genes
CC involved in cellular proliferation, identifying a compound that reduces
CC the activity or level of a gene product required for proliferation of a
CC cell, inhibiting the activity or expression of a gene in an operon
CC required for proliferation, manufacturing an antibiotic, identifying a
CC gene that is required for proliferation of a prokaryotic cell,

CC identifying a compound that inhibits the proliferation of a prokaryotic
CC cell and regulating gene expression in bacteria. The present sequence is
CC a fusion promoter of the invention
XX
SQ Sequence 80 BP; 29 A; 8 C; 8 G; 35 T; 0 U; 0 Other;
Query Match 100.0%; Score 51; DB 8; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATAAAAATTATTTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 51
Db 1 TCATAAAAATTATTTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 51
RESULT 8
ABK98589
ID ABK98589 standard; DNA; 94 BP.
XX
AC ABK98589;
XX
DT 07-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)
XX
DE Xy10-T5 fusion promoter oligonucleotide #1.
XX
KW ss; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;
KW P59; P1P2; PL; xy10; teto; trpO; malO; lambdaclO; cellular proliferation;
KW antibiotic.
XX
OS Eubacteria.
OS Bacteriophage T5.
OS Synthetic.
XX
PN WO200251982-A2.
XX
PD 04-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-US050250.
XX
PR 27-DEC-2000; 2000US-0259434P.
PR 06-SEP-2001; 2001US-00948993.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Wall D, Gross M;
XX
DR WPI; 2002-575374/61.
XX
PT Isolated nucleic acid comprises bacterial promoters modified to have
PT altered activity in at least one gram-positive organism, e.g. Bacillus
PT anthracis or Clostridium botulinum, useful for regulating gene expression
PT in bacteria.
XX
PS Example 1; Page 81; 246pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter comprising at least one promoter that is modified to have
CC altered activity in at least one gram-positive organism, or comprising
CC T5, CP25, P32, P59, P1P2 or PL linked to at least one operator consisting
CC of xy10, teto, trpO, malO or lambdaclO, where at least one operator is
CC positioned so binding of a repressor to an operator represses
CC transcription from the fusion promoter. Also included are vectors and
CC host cells comprising the fusion promoters, a method of identifying genes
CC involved in cellular proliferation or required for proliferation of a
CC prokaryotic cell using the vector, a method of identifying compounds that
CC inhibit the proliferation of a prokaryotic cell using the vector, a
CC method of identifying a compound that reduces the activity or level of a
CC gene product required for proliferation of a cell using the vector, a
CC compound identified by the methods, a method of inhibiting the activity
CC or expression of a gene in an operon required for proliferation using the
CC vector, manufacturing an antibiotic comprising using the vector or cell
CC and identifying a nucleic acid with promoter activity in Enterococcus

CC faecalis. The fusion promoters are useful for regulating nucleic acid or
CC polypeptide expression, particularly for regulating gene expression in
CC bacteria and for identifying proliferation-required genes or molecules
CC with potential antibiotic activity. The modified promoters are also
CC useful for replacing endogenous promoters to create cells with specific
CC regulatable genes. The present sequence is an oligonucleotide used to
CC construct a fusion promoter sequence of the invention. (Updated on 07-AUG
CC -2003 to correct OS field.)
XX
SQ Sequence 94 BP; 35 A; 10 C; 12 G; 37 T; 0 U; 0 Other;
Query Match 100.0%; Score 51; DB 6; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATAAAAATTATTTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 51
Db 6 TCATAAAAATTATTTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 56
RESULT 9
ACD13840
ID ACD13840 standard; DNA; 94 BP.
XX
AC ACD13840;
XX
DT 15-AUG-2003 (first entry)
DT XX
DE Oligonucleotide Xyl-T5.
XX
KW Promoter; ss; gram positive bacteria; Staphylococcus aureus;
KW Enterococcus faecalis; operator; xy10; teto; trpO; malO; lambda-clO;
KW cellular proliferation.
XX
OS Escherichia coli.
OS Synthetic.
OS Unidentified.
XX
PN US2003027286-A1.
XX
PD 06-FEB-2003.
XX
PF 21-DEC-2001; 2001US-00032393.
XX
PR 06-SEP-2000; 2000US-0230335P.
PR 27-DEC-2000; 2000US-0259434P.
XX
PA (HASE/) HASELBECK R.
PA (WALL/) WALL D.
PA (GROS/) GROSS M.
XX
PI Haselbeck R, Wall D, Gross M;
XX
DR WPI; 2003-479541/45.
XX
PT New isolated nucleic acid comprising a fusion promoter having at least
PT one promoter that is modified to have altered activity in at least one
PT gram-positive organism, useful for regulating gene expression in
PT bacteria.
XX
PS Example 1; Page 28; 142pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter having at least one promoter that is modified to have altered
CC activity in at least one gram-positive organism (e.g. Staphylococcus
CC aureus or Enterococcus faecalis). The promoter is linked to at least one
CC operator selected from xy10, teto, trpO, malO and lambda-clO, which are
CC positioned such that the binding of at least one repressor to the
CC operator represses transcription from the fusion promoter. Also included
CC are a vector comprising the isolated nucleic acid, a host cell comprising
CC the nucleic acid. The fusion promoter is useful for identifying genes
CC involved in cellular proliferation, identifying a compound that reduces
CC the activity or level of a gene product required for proliferation of a

CC cell, inhibiting the activity or expression of a gene in an operon
CC required for proliferation, manufacturing an antibiotic, identifying a
CC gene that is required for proliferation of a prokaryotic cell,
CC identifying a compound that inhibits the proliferation of a prokaryotic
CC cell and regulating gene expression in bacteria. The present sequence is
CC an oligonucleotide used in the construction of a fusion promoter of the
CC invention
XX
SQ Sequence 94 BP; 35 A; 10 C; 12 G; 37 T; 0 U; 0 Other;
Query Match 100.0%; Score 51; DB 8; Length 94;
Best Local Similarity 100.0%; Pred.No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATATAAAATTATTTGCTTCAGGAAATTTTCTGTATATAGATTCA 51
Db 6 TCAATAAAATAATTATTTGCTTCAGGAAATTTTCTGTATATAGATTCA 56
RESULT 10
ABK98590/c
ID ABK98590 standard; DNA; 95 BP.
XX
AC ABK98590;
XX
DT 07-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)
XX
DE XylO-T5 fusion promoter oligonucleotide #2.
XX
KW ss; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;
KW P59; P1P2; PL; xylO; tetO; trpO; malO; lambdaclO; cellular proliferation;
KW antibiotic.
XX
OS Eubacteria.
OS Bacteriophage T5.
OS Synthetic.
XX
PN WO200251982-A2.
XX
PD 04-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-US050250.
XX
PR 27-DEC-2000; 2000US-0259434P.
PR 06-SEP-2001; 2001US-00948993.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Wall D, Gross M;
XX
DR WPI; 2002-575374/61.
XX
PT Isolated nucleic acid comprises bacterial promoters modified to have
PT altered activity in at least one gram-positive organism, e.g. Bacillus
PT anthracis or Clostridium botulinum, useful for regulating gene expression
PT in bacteria.
XX
PS Example 1; Page 81; 246pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter comprising at least one promoter that is modified to have
CC altered activity in at least one gram-positive organism, or comprising
CC T5, CP25, P32, P59, P1P2 or PL linked to at least one operator consisting
CC of xylO, tetO, trpO, malO or lambdaclO, where at least one operator is
CC positioned so binding of a repressor to an operator represses
CC transcription from the fusion promoter. Also included are vectors and
CC host cells comprising the fusion promoters, a method of identifying genes
CC involved in cellular proliferation or required for proliferation of a
CC prokaryotic cell using the vector, a method of identifying compounds that
CC inhibit the proliferation of a prokaryotic cell using the vector, a
CC method of identifying a compound that reduces the activity or level of a
CC gene product required for proliferation of a cell using the vector, a

CC compound identified by the methods, a method of inhibiting the activity
CC or expression of a gene in an operon required for proliferation using the
CC vector, manufacturing an antibiotic comprising using the vector or cell
CC and identifying a nucleic acid with promoter activity in Enterococcus
CC faecalis. The fusion promoters are useful for regulating nucleic acid or
CC polypeptide expression, particularly for regulating gene expression in
CC bacteria and for identifying proliferation-regulated genes or molecules
CC with potential antibiotic activity. The modified promoters are also
CC useful for replacing endogenous promoters to create cells with specific
CC regulatable genes. The present sequence is an oligonucleotide used to
CC construct a fusion promoter sequence of the invention. (Updated on 07-AUG
CC -2003 to correct OS field.)
XX
SQ Sequence 95 BP; 39 A; 11 C; 9 G; 36 T; 0 U; 0 Other;
Query Match 100.0%; Score 51; DB 6; Length 95;
Best Local Similarity 100.0%; Pred.No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATATAAAATTATTTGCTTCAGGAAATTTTCTGTATATAGATTCA 51
Db 93 TCAATAAAATAATTATTTGCTTCAGGAAATTTTCTGTATATAGATTCA 43
RESULT 11
ACD13841/c
ID ACD13841 standard; DNA; 95 BP.
XX
AC ACD13841;
XX
DT 15-AUG-2003 (first entry)
XX
DE Oligonucleotide Xyl-T5 complement.
XX
KW Promoter; ss; gram positive bacteria; Staphylococcus aureus;
KW Enterococcus faecalis; operator; xylO; tetO; trpO; malO; lambda-clO;
KW cellular proliferation.
XX
OS Escherichia coli.
OS Synthetic.
OS Unidentified.
XX
PN US2003027286-A1.
XX
PD 06-FEB-2003.
XX
PF 21-DEC-2001; 2001US-00032393.
XX
PR 06-SEP-2000; 2000US-0230335P.
PR 27-DEC-2000; 2000US-0259434P.
XX
PA (HASE/) HASELBECK R.
PA (WALL/) WALL D.
PA (GROS/) GROSS M.
XX
PI Haselbeck R, Wall D, Gross M;
XX
DR WPI; 2003-479541/45.
XX
PT New isolated nucleic acid comprising a fusion promoter having at least
PT one promoter that is modified to have altered activity in at least one
PT gram-positive organism, useful for regulating gene expression in
PT bacteria.
XX
PS Example 1; Page 28; 142pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter having at least one promoter that is modified to have altered
CC activity in at least one gram-positive organism (e.g. Staphylococcus
CC aureus or Enterococcus faecalis). The promoter is linked to at least one
CC operator selected from xylO, tetO, trpO, malO and lambda-clO, which are
CC positioned such that the binding of at least one repressor to the
CC operator represses transcription from the fusion promoter. Also included

PF 08-AUG-1988; 88EP-00112864.
XX
PR 17-AUG-1987; 87CH-00003152.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
XX
PI Bujard H, Lanzer M;
XX
DR WPI; 1989-055375/08.
XX
PT Deoxyribonucleic acid data expression control sequences - comprising
PT Promoter and operator-repressor-sequences.
XX
PS Disclosure; Fig 7; 65pp; German.
XX
CC Sequence is the operator/promoter N25OP29 and is inserted into plasmid
CC pDS3 for expression of a variety of proteins from pro- and eukaryotic
CC sources. It is prepared as a DNA XhoI/EcoRI frag. It comprises a low
CC signal strength/high promoter strength promoter and high complexing rate
CC operator/repressor. It gives high transcription and translation efficienc
CC ies and good repressability. See also AAN91060, 1,2,3,5,6,8 and AAN91070.
CC (Updated on 03-OCT-2002 to add missing OS field.)
XX
SQ Sequence 207 BP; 66 A; 37 C; 37 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51
124 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATATAGATTCA 174

RESULT 15

AAN60259
ID AAN60259 standard; DNA; 247 BP.

XX AAN60259;

DT 27-AUG-2003 (revised)
DT 29-MAY-1991 (first entry)

XX Coliphage PN25 Pre-early promoter of plasmid pDS1, PN25, tol+.

XX DHFR; chloramphenicol acetyl-transferase; malaria SA; IL-2; IFN; insulin;
XX tPA; renin.

XX Unidentified.

XX EPI86069-A.

XX 02-JUL-1986.

XX 13-DEC-1985; 85EP-00115921.

XX 17-DEC-1984; 84GB-00031818.

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX Bujard H, Stuber D;

XX WPI; 1986-170629/27.

PT Expression control DNA sequence - comprising T5 promoter combined with
PT DNA sequence which permits control of promoter activity.

XX Disclosure; Fig 2; 26pp; English.

XX Plasmid vectors of the pDS1 family may be used to express a sequence
CC under the control of a coliphage T5 promoter eg. the coliphage PN25 pre-
CC early promoter, and one or more sequences which allow control of the
CC promoter. Sequences expressed include products such as dihydrofolate

CC reductase; chloramphenicol acetyl-transferase; malaria surface antigen;
CC IL-2; IFN-alpha, -beta and -gamma; insulin; growth hormones; tPA; human
CC renin etc. (Updated on 27-AUG-2003 to correct OS field.)
XX

SQ Sequence 247 BP; 79 A; 44 C; 48 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51
124 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATATAGATTCA 174

Search completed: April 7, 2004, 04:23:52
Job time : 246 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2004, 04:19:50 ; Search time 52 Seconds
(without alignments)
544.279 Million cell updates/sec

Title: US-10-032-393-36
Perfect score: 51
Sequence: 1 tcaataaaatttatttgc.....tttctgataatagattca 51

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.4	65.5	125	1	US-08-400-864-2
2	33	64.7	171	2	US-08-892-272-3
3	33	64.7	757	2	US-08-892-272-1
4	31.4	61.6	49	1	US-08-400-864-1
5	28.6	56.1	247	3	US-09-344-888A-24
6	28.6	56.1	250	3	US-08-840-468A-25
7	28.6	56.1	250	4	US-09-696-188B-25
8	28.6	56.1	520	1	US-08-268-348A-7
9	28.6	56.1	520	1	US-08-268-348A-9
10	28.6	56.1	1106	1	US-08-041-648-4
11	28.6	56.1	1106	1	US-08-041-648-6
12	28.6	56.1	1106	1	US-08-041-648-8
13	28.6	56.1	3462	4	US-09-742-373-10
14	28.6	56.1	3977	1	US-07-794-400-2
15	28.6	56.1	3977	1	US-07-794-400-13
16	28.6	56.1	3977	1	US-08-041-648-1
17	28.6	56.1	3977	1	US-08-217-529-1
18	28.6	56.1	3977	1	US-08-397-470-2
19	28.6	56.1	3977	1	US-08-397-470-13
20	28.6	56.1	4491	4	US-09-483-419-2
21	28.6	56.1	4491	4	US-09-837-863-23
22	28.6	56.1	4755	4	US-09-837-863-24
23	28.6	56.1	6501	4	US-09-767-515-1
24	28.6	56.1	6501	4	US-09-767-515-2
25	27.2	53.3	1830121	4	US-09-557-884-1
26	27.2	53.3	1830121	4	US-09-643-990A-1

C	28	25.4	49.8	843	4	US-09-134-001C-2669	Sequence 2669, Ap
	29	25	49.0	92407	4	US-09-596-002-36	Sequence 36, Appl
	30	25	49.0	640681	4	US-09-790-988-1	Sequence 1, Appli
C	31	24.8	48.6	6152	3	US-08-973-462-1	Sequence 1, Appli
C	32	24.4	47.8	2728	4	US-09-620-312D-572	Sequence 572, App
C	33	24.4	47.8	15788	4	US-09-920-759-13	Sequence 13, Appl
	34	24.4	47.8	193303	4	US-09-497-855A-37	Sequence 37, Appl
	35	24.4	47.8	193303	4	US-09-497-855A-44	Sequence 44, Appl
	36	24.2	47.5	1650	4	US-09-907-794A-254	Sequence 254, App
	37	24.2	47.5	1650	4	US-09-905-125A-254	Sequence 254, App
	38	24.2	47.5	1650	4	US-09-902-775A-254	Sequence 254, App
C	39	24	47.1	640681	4	US-09-790-988-1	Sequence 1, Appli
	40	23.8	46.7	786431	4	US-09-751-389-3	Sequence 3, Appli
	41	23.6	46.3	2243	1	US-07-995-657-1	Sequence 1, Appli
	42	23.6	46.3	2243	1	US-08-474-587-1	Sequence 1, Appli
	43	23.6	46.3	2249	2	US-08-974-546-2	Sequence 2, Appli
	44	23.6	46.3	6113	4	US-10-204-708-14	Sequence 14, Appli
C	45	23.6	46.3	112132	4	US-09-741-150-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-400-864-2
Sequence 2, Application US/08400864
Patent No. 5721137
GENERAL INFORMATION:
APPLICANT: FRASCOTI, GIANNI
APPLICANT: GRANDI, GUIDO
TITLE OF INVENTION: PLASMID VECTOR AND ITS USE FOR THE
TITLE OF INVENTION: PRODUCTION OF HETEROLOGOUS PROTEINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400, 864
FILING DATE: 08-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT 000727 MI94A
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2264-083-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-400-864-2
Query Match 65.5%; Score 33.4; DB 1; Length 125;
Best local Similarity 95.7%; Pred. No. 0.16;
Matches 45; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 6 AAAAAATTATTTGCTTCAGGAAA-TTTTYCTGTATTAATACATTC 51
| | | | | | | | | | | | | | | | | | | | | |
Db 5 AAAAAATTATTTGCTTCAGGAAAATTTTTATGTATAATACATTC 51

RESULT 2

```

US-08-892-272-3
; Sequence 3, Application US/08892272
; Patent No. 5891687
;
; GENERAL INFORMATION:
;   APPLICANT: SCHLIEPER, Daniel
;   APPLICANT: SOBEK, Harald
;   APPLICANT: SCHMIDT, Manfred
;   APPLICANT: VON WILKEN-BERGMAN, Brigitte
;   APPLICANT: MULLER-HILL, Benno
;   TITLE OF INVENTION: POSITIVE SELECTION VECTOR BASED ON THE
;   TITLE OF INVENTION: CAPS GENE, PCAPS VECTOR AND ITS USE
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
;   STREET: 655 Fifteenth Street N.W. Suite 330
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20005-5701
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentln Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/892,272
;   FILING DATE: 14-JUL-1997
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: DE 196 30 617.5
;   FILING DATE: 29-JUL-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Murray, Robert B.
;   REGISTRATION NUMBER: 22,980
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202)638-5000
;   TELEFAX: (202)638-4810
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 171 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-08-892-272-3

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Query Match	64.7%;	Score 33;	DB 2;	Length 171;
Best Local Similarity	79.6%;	Pred. No. 0.21;		
Matches 39;	Conservative	0;	Mismatches 10;	Indels 0;
				Gaps 0;

QY 3 ATAAAAAATTATTGCTTTCAGAAAAATTTTCTGTATAATAGATTCA 51
|||||
71 ATAAAAAATTATTGCTTTCAGGTACAATTCGTATATAATATTATCA 119
Db

RESULT 3

US-08-892-272-1
; Sequence 1, Application US/08892272
; Patent No. 5891687
; GENERAL INFORMATION:
; APPLICANT: SCHLIEPER, Daniel
; APPLICANT: SOBEK, Harald
; APPLICANT: SCHMIDT, Manfred
; APPLICANT: VON WILKEN-BERGEMANN, Brigitte

```

1  NUMBER OF SEQUENCES: 5
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
4  STREET: 655 Fifteenth Street N.W. Suite 330
5  CITY: Washington
6  STATE: D.C.
7  COUNTRY: U.S.A.
8  ZIP: 20005-5701
9  COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: PatentIn Release #1.0, Version #1.30
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/892,272
16 FILING DATE: 14-JUL-1997
17 CLASSIFICATION: 435
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: DE 196 30 617.5
20 FILING DATE: 29-JUL-1996
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Murray, Robert B.
23 REGISTRATION NUMBER: 22,980
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (202)638-5000
26 TELEFAX: (202)638-4810
27 INFORMATION FOR SEQ ID NO: 1:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 757 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33 MOLECULE TYPE: DNA (genomic)
34 FEATURE:
35 NAME/KEY: CDS
36 LOCATION: 90..722
37
38 US-08-892-272-1

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Query Match	64.78;	Score 33;	DB 2;	Length 757;
Best Local Similarity	79.68;	Pred. No. 0.22;		
Matches 39;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;

QY 3 ATAAAAAATTATTTGCTTTCAGGAATTTTCTGTATAATAGATTCA 51
 |||||
DB 13 ATAAAAAATTATTTGCTTTCAGGTACAATTTCTGTATAATATTATCA 61

RESULT 4

US-08-400-864-1
; Sequence 1, Application US/08400864
; Patent No. 5721137

GENERAL INFORMATION:
APPLICANT: FRASCOTTI, GIANNI
APPLICANT: GRANDI, GUIDO
TITLE OF INVENTION: PLASMID VECTOR AND ITS USE FOR THE
TITLE OF INVENTION: PRODUCTION OF HETEROLOGOUS PROTEINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR

CITY: ARLINGTON
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COUNTRY: U
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT 000727 M194A
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2264-083-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-400-864-1

Query Match 61.6%; Score 31.4; DB 1; Length 49;
Best Local Similarity 95.6%; Pred. No. 0.57;
Matches 43; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 6 AAAAATTATTTGCTTCAGGAAA-TTTTCTGTATATAGATT 49
|||||
DB 5 AAAATTATTGCTTCAGGAAATTTTATGTATATAGATT 49

RESULT 5
US-09-344-888A-24
Sequence 24, Application US/09344888A
Patent No. 6291245
GENERAL INFORMATION:
APPLICANT: Kopetzki, Erhard
APPLICANT: Schantz, Christian
TITLE OF INVENTION: New Host-Vector System
FILE REFERENCE: CD20315
CURRENT APPLICATION NUMBER: US/09/344,888A
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: EP98113156.8
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: EP98119078.8
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 247
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:expression cassette
US-09-344-888A-24

Query Match 56.1%; Score 28.6; DB 3; Length 247;
Best Local Similarity 72.5%; Pred. No. 3.8;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTTGCTTCAGGAAATTTTCTGTATATAGATTCA 51
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DB 10 TCATAAAAAATTATTTGCTTCAGGCGGATACCAATTATATAGATTCA 60

RESULT 6
US-08-840-466A-25
Sequence 25, Application US/08840466A
Patent No. 6261561
GENERAL INFORMATION:
APPLICANT: Stewart, C. Neal
McKee, Marian L.
O'Brien, Alison D.
Wachtel, Marian P

By Administration Of Host Organisms That Express Intimin
Alone Or As A Fusion Protein With One Or More Other
Antigens.

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner, L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,466A
FILING DATE: 18-Apr-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Boone, Laura L S.
REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 04995.0029-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-840-466A-25

Query Match 56.1%; Score 28.6; DB 3; Length 250;
Best Local Similarity 72.5%; Pred. No. 3.8;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTTGCTTCAGGAAATTTTCTGTATATAGATTCA 51
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DB 10 TCATAAAAAATTATTTGCTTCAGGCGGATACCAATTATATAGATTCA 60

RESULT 7
US-09-696-188B-25
Sequence 25, Application US/09696188B
Patent No. 6406885
GENERAL INFORMATION:
APPLICANT: Stewart, C. Neal
McKee, Marian L.
O'Brien, Alison D.
Wachtel, Marian R.
TITLE OF INVENTION: Method Of Stimulating An Immune Response
By Administration Of Host Organisms That Express Intimin
Alone Or As A Fusion Protein With One Or More Other
Antigens.

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner, L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/696,188B
FILING DATE: 26-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/840,466
FILING DATE: 1997-04-18
ATTORNEY/AGENT INFORMATION:
NAME: Boone, Laura L S.
REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 04995.0029-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-696-188B-25

Query Match 56.1%; Score 28.6; DB 4; Length 250;
Best Local Similarity 72.5%; Pred. No. 3.8;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 TCATATAAAATTATTTGCTTCAGGAAATTTTCGTATATAGATTCA 51
10 TCATATAAAATTATTTGCTTCGTTCGACCGGATACACATTATAATAGATTCA 60
DB

RESULT 8
US-08-268-348A-7
Sequence 7, Application US/08268348A
Patent No. 5750374
GENERAL INFORMATION:
APPLICANT: Dobelli, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotzman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
TITLE OF INVENTION: Producing Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326

TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 115..516
OTHER INFORMATION: /product= "Amyloid Protein AA"
US-08-268-348A-7

Query Match 56.1%; Score 28.6; DB 1; Length 520;
Best Local Similarity 72.5%; Pred. No. 4;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 TCATATAAAATTATTTGCTTCAGGAAATTTTCGTATATAGATTCA 51
10 TCATATAAAATTATTTGCTTCGTTCGACCGGATACACATTATAATAGATTCA 60
DB

RESULT 9
US-08-268-348A-9
Sequence 9, Application US/08268348A
Patent No. 5750374
GENERAL INFORMATION:
APPLICANT: Dobelli, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotzman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
TITLE OF INVENTION: Producing Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 115..516

OTHER INFORMATION: /product= "Amyloid Protein AA"
US-08-268-348A-9

Query Match 56.1%; Score 28.6; DB 1; Length 520;
Best Local Similarity 72.5%; Pred. No. 4;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 1 TCATAAAAAATTATTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51
10 TCATAAAAAATTATTGCTTCAGGCGGATTAACAATTATAATAGATTCA 60

RESULT 10
US-08-041-648-4
; Sequence 4, Application US/08041648
; Patent No. 5486463
; GENERAL INFORMATION:

APPLICANT: Lesslauer, Werner
APPLICANT: L tscher, Hansruedi
APPLICANT: St ber, Dietrich
TITLE OF INVENTION: TNF-MUTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110-1199

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/041,648
FILING DATE: 1-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92810249.0
FILING DATE: 2-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, Catherine R.
REGISTRATION NUMBER: 34240
REFERENCE/DOCKET NUMBER: RAN 4105/147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1106 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Plasmid pDS56/RBSII, SphI-TNFalpha(Trp32)
FEATURE:
NAME/KEY: CDS
LOCATION: 994..1104
US-08-041-648-4

Query Match 56.1%; Score 28.6; DB 1; Length 1106;
Best Local Similarity 72.5%; Pred. No. 4.1;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 1 TCATAAAAAATTATTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51
886 TCATAAAAAATTATTGCTTCAGGCGGATTAACAATTATAATAGATTCA 936

RESULT 11

US-08-041-648-6
; Sequence 6, Application US/08041648
; Patent No. 5486463
; GENERAL INFORMATION:

APPLICANT: Lesslauer, Werner
APPLICANT: L tscher, Hansruedi
APPLICANT: St ber, Dietrich
TITLE OF INVENTION: TNF-MUTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110-1199

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/041,648
FILING DATE: 1-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92810249.0
FILING DATE: 2-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, Catherine R.
REGISTRATION NUMBER: 34240
REFERENCE/DOCKET NUMBER: RAN 4105/147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1106 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Plasmid pDS56/RBSII, SphI-TNFalpha(Ser29)
FEATURE:
NAME/KEY: CDS
LOCATION: 994..1104
US-08-041-648-6

Query Match 56.1%; Score 28.6; DB 1; Length 1106;
Best Local Similarity 72.5%; Pred. No. 4.1;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 1 TCATAAAAAATTATTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51
886 TCATAAAAAATTATTGCTTCAGGCGGATTAACAATTATAATAGATTCA 936

RESULT 12

US-08-041-648-8
; Sequence 8, Application US/08041648
; Patent No. 5486463
; GENERAL INFORMATION:

APPLICANT: Lesslauer, Werner
APPLICANT: L tscher, Hansruedi
APPLICANT: St ber, Dietrich
TITLE OF INVENTION: TNF-MUTEINS
NUMBER OF SEQUENCES: 17

```

CORRESPONDENCE ADDRESS:
ADDRESS: George M. Gould, Esq., Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110-1199

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/041,648
FILING DATE: 1-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92810249.0
FILING DATE: 2-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, Catherine R.
REGISTRATION NUMBER: 34240
REFERENCE/DOCKET NUMBER: RAN 4105/147
TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1106 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Plasmid pDS56/RBSII,SphI-TNFalpha(Ser29Tyr32)
FEATURE:
NAME/KEY: CDS
LOCATION: 994..1104
US-08-041-648-8

Query Match
Best Local Similarity 56.1%; Score 28.6; DB 1; Length 1106;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 TCATATAAAATTATTTGCTTTCAGAAATTTTCTGTATATAGATTCA 51
Db 886 TCATATAAAATTATTTGCTTGTGAGCGATTAACAATTATATAGATTCA 936

RESULT 13
US-09-742-373-10
Sequence 10, Application US/09742373
Patent No. 6562946
GENERAL INFORMATION:
APPLICANT: Althaus, Harald
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: Human Procalcitonin and the Preparation and Use Thereof
FILE REFERENCE: 05552.1445-00
CURRENT APPLICATION NUMBER: US/09/742,373
PRIOR APPLICATION NUMBER: 2000-12-22
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 10016278.9
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: 10027954.6
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 3462
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TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Vectorsequence ,
US-09-742-373-10

Query Match
Best Local Similarity 56.1%; Score 28.6; DB 4; Length 3462;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 TCATATAAAATTATTTGCTTTCAGAAATTTTCTGTATATAGATTCA 51
Db 10 TCATATAAAATTATTTGCTTGTGAGCGATTAACAATTATATAGATTCA 60

RESULT 14
US-07-794-400-2
Sequence 2, Application US/07794400
Patent No. 5422104
GENERAL INFORMATION:
APPLICANT: Fiers, W.
APPLICANT: Tavernier, J.
APPLICANT: Van Ostade, X.
TITLE OF INVENTION: TNF-Mutlains
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/794,400
FILING DATE: 19911120
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90810901.0
FILING DATE: 21-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Krovatin, William
REGISTRATION NUMBER: 33256
REFERENCE/DOCKET NUMBER: 4105/136-00
TELEPHONE: (201) 235-4387
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3977 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (recombinant plasmid)
IMMEDIATE SOURCE:
CLONE: pDS56/RBSII,SphI-TNF-alpha
FEATURE:
NAME/KEY: CDS
LOCATION: 115..591
US-07-794-400-2

Query Match
Best Local Similarity 56.1%; Score 28.6; DB 1; Length 3977;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 TCATATAAAATTATTTGCTTTCAGAAATTTTCTGTATATAGATTCA 51
Db 10 TCATATAAAATTATTTGCTTGTGAGCGATTAACAATTATATAGATTCA 60
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2004, 04:12:30 ; Search time 1006 Seconds
(without alignments)
189.995 Million cell updates/sec

Title: US-10-032-393-36
Perfect score: 51
Sequence: 1 tcataaaaaatttatttgcgt.....tttctgtataatagattca 51

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Gapop 10.0 , Gapext 1.0

Searched: 2470632 segs, 1873875610 residues

Total number of hits satisfying chosen parameters: 4941264

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	51	100.0	72	9	US-09-788-297-6
3	51	100.0	80	9	US-09-788-297-7
4	51	100.0	80	14	US-10-032-393-26
5	51	100.0	94	14	US-10-032-393-5
6	51	100.0	95	14	US-10-032-393-6
7	51	100.0	556	14	US-10-032-393-1
8	51	100.0	5302	15	US-10-385-415-2
9	51	100.0	5767	15	US-10-385-415-4
10	51	100.0	6852	14	US-10-032-393-16
11	50	84.3	1246	9	US-09-815-242-3094
12	43	84.3	51	14	US-10-032-393-37
13	43	84.3	80	14	US-10-032-393-27
14	43	84.3	94	14	US-10-032-393-22
15	43	84.3	95	14	US-10-032-393-23

16	43	84.3	6852	14	US-10-032-393-53	Sequence 53, Appl
17	29.8	58.4	113515	14	US-10-311-455-2148	Sequence 2148, Ap
18	28.6	56.1	82	14	US-10-288-858-13	Sequence 13, Appl
19	28.6	56.1	94	14	US-10-032-393-12	Sequence 12, Appl
20	28.6	56.1	95	14	US-10-032-393-13	Sequence 13, Appl
21	28.6	56.1	134	14	US-10-284-083-3	Sequence 3, Appl
22	28.6	56.1	138	14	US-10-284-083-4	Sequence 4, Appl
23	28.6	56.1	138	14	US-10-284-083-5	Sequence 5, Appl
24	28.6	56.1	162	9	US-09-828-523A-97	Sequence 97, Appl
25	28.6	56.1	162	10	US-09-966-521-89	Sequence 89, Appl
26	28.6	56.1	162	14	US-10-429-094-89	Sequence 89, Appl
27	28.6	56.1	166	14	US-10-284-083-2	Sequence 2, Appl
28	28.6	56.1	170	14	US-10-284-083-6	Sequence 6, Appl
29	28.6	56.1	250	8	US-08-837-459-25	Sequence 25, Appl
30	28.6	56.1	250	14	US-10-150-058-25	Sequence 25, Appl
31	28.6	56.1	2220	14	US-10-288-858-5	Sequence 5, Appl
32	28.6	56.1	3420	15	US-10-385-415-1	Sequence 1, Appl
33	28.6	56.1	3462	9	US-09-742-373-10	Sequence 10, Appl
34	28.6	56.1	3462	14	US-10-394-058-10	Sequence 10, Appl
35	28.6	56.1	3876	15	US-10-385-415-27	Sequence 27, Appl
36	28.6	56.1	3876	15	US-10-385-415-28	Sequence 28, Appl
37	28.6	56.1	3879	15	US-10-385-415-5	Sequence 5, Appl
38	28.6	56.1	3879	15	US-10-385-415-6	Sequence 6, Appl
39	28.6	56.1	3879	15	US-10-385-415-7	Sequence 7, Appl
40	28.6	56.1	3879	15	US-10-385-415-21	Sequence 21, Appl
41	28.6	56.1	3879	15	US-10-385-415-25	Sequence 25, Appl
42	28.6	56.1	3879	15	US-10-385-415-26	Sequence 26, Appl
43	28.6	56.1	3885	15	US-10-385-415-3	Sequence 3, Appl
44	28.6	56.1	3897	15	US-10-385-415-20	Sequence 20, Appl
45	28.6	56.1	3900	15	US-10-385-415-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-10-032-393-36

Sequence 36, Application US/10032393

Publication No. US20030027286A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Wall, Daniel

APPLICANT: Gross, Molly

TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE

FILE REFERENCE: ELITRA.010A

CURRENT APPLICATION NUMBER: US/10/032,393

PRIOR FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 60/259,434

PRIOR FILING DATE: 2000-12-27

PRIOR APPLICATION NUMBER: 09/948,993

PRIOR FILING DATE: 2001-09-06

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 36

LENGTH: 51

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Xyl-T5 promoter sequence

US-10-032-393-36

Query Match 100.0%; Score 51; DB 14; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAAAATTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51
DB 1 TCATAAAAAATTATTTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51

RESULT 2

US-09-788-297-6

```
/ Sequence 6, Application US/09788297
/ Patent No. US20020094516A1
/ GENERAL INFORMATION:
/ APPLICANT: Calos, Michele P.
/ APPLICANT: Scilmenti, Christopher R.
/ TITLE OF INVENTION: ALTERED RECOMBINASES FOR GENOME MODIFICATION
/ FILE REFERENCE: 8400-0011
/ CURRENT APPLICATION NUMBER: US/09/788,297
/ CURRENT FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 72
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:TS, oligo 1
US-09-788-297-6
```

```
Query Match          100.0%; Score 51; DB 9; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 51

Db 2 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 52

RESULT 3

US-09-788-297-7/c

```
/ Sequence 7, Application US/09788297
/ Patent No. US20020094516A1
/ GENERAL INFORMATION:
/ APPLICANT: Calos, Michele P.
/ APPLICANT: Scilmenti, Christopher R.
/ TITLE OF INVENTION: ALTERED RECOMBINASES FOR GENOME MODIFICATION
/ FILE REFERENCE: 8400-0011
/ CURRENT APPLICATION NUMBER: US/09/788,297
/ CURRENT FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 80
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:TS, oligo 2
US-09-788-297-7
```

```
Query Match          100.0%; Score 51; DB 9; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 51

Db 75 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 25

RESULT 4

US-10-032-393-26

```
/ Sequence 26, Application US/10032393
/ Publication No. US20030027286A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Wall, Daniel
/ APPLICANT: Gross, Molly
/ TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
/ FILE REFERENCE: ELITRA.010A
/ CURRENT APPLICATION NUMBER: US/10/032,393
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 60/259,434
/ PRIOR FILING DATE: 2000-12-27
```

```
/ PRIOR APPLICATION NUMBER: 09/948,993
/ PRIOR FILING DATE: 2001-09-06
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ NUMBER OF SEQ ID NOS: 68
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 26
/ LENGTH: 80
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Xyl-T5 fusion sequence
US-10-032-393-26
```

```
Query Match          100.0%; Score 51; DB 14; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 51

Db 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 51

RESULT 5

US-10-032-393-5

```
/ Sequence 5, Application US/10032393
/ Publication No. US20030027286A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Wall, Daniel
/ APPLICANT: Gross, Molly
/ TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
/ FILE REFERENCE: ELITRA.010A
/ CURRENT APPLICATION NUMBER: US/10/032,393
/ PRIOR FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 60/259,434
/ PRIOR FILING DATE: 2000-12-27
/ PRIOR APPLICATION NUMBER: 09/948,993
/ PRIOR FILING DATE: 2001-09-06
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ NUMBER OF SEQ ID NOS: 68
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 94
/ TYPE: DNA
/ ORGANISM: Escherichia coli
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide Xyl-T5
US-10-032-393-5
```

```
Query Match          100.0%; Score 51; DB 14; Length 94;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 51

Db 6 TCATAAAAAATTATTTGCTTTCAGGAAATTTTCTGTATAATAGATTCA 56

RESULT 6

US-10-032-393-6/c

```
/ Sequence 6, Application US/10032393
/ Publication No. US20030027286A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Wall, Daniel
/ APPLICANT: Gross, Molly
/ TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
/ FILE REFERENCE: ELITRA.010A
/ CURRENT APPLICATION NUMBER: US/10/032,393
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 60/259,434
```

; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/948,993
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Xyl-T5 complement
US-10-032-393-6

Query Match 100.0%; Score 51; DB 14; Length 95;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAATTTATTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51
|||||
Db 93 TCATAAAATTTATTGCTTCAGGAAATTTTCTGTATAATAGATTCA 43

RESULT 7

US-10-032-393-1
; Sequence 1, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Wall, Daniel
; APPLICANT: Gross, Molly
; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
; FILE REFERENCE: ELITRA.010A
; CURRENT APPLICATION NUMBER: US/10/032,393
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/259,434
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/948,993
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence map showing the Xyl-T5 fusion promoter
US-10-032-393-1

Query Match 100.0%; Score 51; DB 14; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAATTTATTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51
|||||
Db 6 TCATAAAATTTATTGCTTCAGGAAATTTTCTGTATAATAGATTCA 56

RESULT 8

US-10-385-415-2
; Sequence 2, Application US/10385415
; Publication No. US20040014158A1
; GENERAL INFORMATION:
; APPLICANT: Bacher, Adelbert
; APPLICANT: Fischer, Markus
; TITLE OF INVENTION: PRODUCING THEM, THEIR USE AND MEDICAMENTS AND VACCINES CONTAININ
; TITLE OF INVENTION: A CERTAIN QUANTITY OF SAID PROTEIN CONJUGATES
; FILE REFERENCE: 9286.6CT

; CURRENT APPLICATION NUMBER: US/10/385,415
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 09/936,028
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/EP00/01899
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: DE 19910102.7
; PRIOR FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 5302
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: p6021-CAT Expression vector
US-10-385-415-2

Query Match 100.0%; Score 51; DB 15; Length 5302;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAATTTATTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51
|||||
Db 134 TCATAAAATTTATTGCTTCAGGAAATTTTCTGTATAATAGATTCA 184

RESULT 9

US-10-385-415-4
; Sequence 4, Application US/10385415
; Publication No. US20040014158A1
; GENERAL INFORMATION:
; APPLICANT: Bacher, Adelbert
; APPLICANT: Fischer, Markus
; TITLE OF INVENTION: PROTEIN CONJUGATES, METHOD, VECTORS, PROTEINS AND DNA FOR
; TITLE OF INVENTION: PRODUCING THEM, THEIR USE AND MEDICAMENTS AND VACCINES CONTAININ
; TITLE OF INVENTION: A CERTAIN QUANTITY OF SAID PROTEIN CONJUGATES
; FILE REFERENCE: 9286.6CT
; CURRENT APPLICATION NUMBER: US/10/385,415
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 09/936,028
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/EP00/01899
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: DE 19910102.7
; PRIOR FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 5767
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: p602-Bs-lusY Expression plasmid
US-10-385-415-4

Query Match 100.0%; Score 51; DB 15; Length 5767;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAAAATTTATTGCTTCAGGAAATTTTCTGTATAATAGATTCA 51
|||||
Db 134 TCATAAAATTTATTGCTTCAGGAAATTTTCTGTATAATAGATTCA 184

RESULT 10

US-10-032-393-16
; Sequence 16, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Wall, Daniel
; APPLICANT: Gross, Molly

;; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
;; FILE REFERENCE: ELITRA.010A
;; CURRENT APPLICATION NUMBER: US/10/032,393
;; CURRENT FILING DATE: 2001-12-21
;; PRIOR APPLICATION NUMBER: 60/259,434
;; PRIOR FILING DATE: 2000-12-27
;; PRIOR APPLICATION NUMBER: 09/948,993
;; PRIOR FILING DATE: 2001-09-06
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; NUMBER OF SEQ ID NOS: 68
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 16
;; LENGTH: 6852
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Vector pXyl-T5 p15a
US-10-032-393-16

Query Match 100.0%; Score 51; DB 14; Length 6852;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATATAAAATTTATTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51
Db 1367 TCATATAAAATTTATTGCTTTCAGGAAATTTTCTGTATATAGATTCA 1417

RESULT 11

US-09-815-242-3094
;; Sequence 3094, Application US/09815242
;; Patent No. US20020061569A1
;; GENERAL INFORMATION:
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Kari L.
;; APPLICANT: Zyskind, Judith W.
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John D.
;; APPLICANT: Carr, Grant J.
;; APPLICANT: Yamamoto, Robert T.
;; APPLICANT: Xu, H. Howard
;; TITLE OF INVENTION: Identification of Essential Genes in
;; FILE REFERENCE: ELITRA.011A
;; CURRENT APPLICATION NUMBER: US/09/815,242
;; CURRENT FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3094
;; LENGTH: 1246
;; TYPE: DNA
;; ORGANISM: Staphylococcus aureus
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)...(1246)
;; OTHER INFORMATION: n = A,T,C or G
US-09-815-242-3094

Query Match 98.0%; Score 50; DB 9; Length 1246;
Best Local Similarity 98.0%; Pred. No. 6.3e-05;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATATAAAATTTATTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51
Db 13 TCATATAAAATTTATTGCTTTCAGGAAATTTTCTGTATATAGATTCA 63

RESULT 12

US-10-032-393-37
;; Sequence 37, Application US/10032393
;; Publication No. US20030027286A1
;; GENERAL INFORMATION:
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Wall, Daniel
;; APPLICANT: Gross, Molly
;; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
;; FILE REFERENCE: ELITRA.010A
;; CURRENT APPLICATION NUMBER: US/10/032,393
;; CURRENT FILING DATE: 2001-12-21
;; PRIOR APPLICATION NUMBER: 60/259,434
;; PRIOR FILING DATE: 2000-12-27
;; PRIOR APPLICATION NUMBER: 09/948,993
;; PRIOR FILING DATE: 2001-09-06
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; NUMBER OF SEQ ID NOS: 68
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 37
;; LENGTH: 51
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Xyl-T5-DD promoter sequence
US-10-032-393-37

Query Match 84.3%; Score 43; DB 14; Length 51;
Best Local Similarity 90.2%; Pred. No. 0.0033;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCATATAAAATTTATTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51
Db 1 TCATATAAAATTTATTGCTTTCAGGAAATTTTCTGTATATAGATTCA 51

RESULT 13

US-10-032-393-27
;; Sequence 27, Application US/10032393
;; Publication No. US20030027286A1
;; GENERAL INFORMATION:
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Wall, Daniel
;; APPLICANT: Gross, Molly
;; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
;; FILE REFERENCE: ELITRA.010A
;; CURRENT APPLICATION NUMBER: US/10/032,393
;; CURRENT FILING DATE: 2001-12-21
;; PRIOR APPLICATION NUMBER: 60/259,434
;; PRIOR FILING DATE: 2000-12-27
;; PRIOR APPLICATION NUMBER: 09/948,993
;; PRIOR FILING DATE: 2001-09-06
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; NUMBER OF SEQ ID NOS: 68
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 27
;; LENGTH: 80
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Xyl-T5-DD fusion sequence
US-10-032-393-27

Query Match	84.3%	Score 43;	DB 14;	Length 80;
Best Local Similarity	90.2%;	Pred. No. 0.0036;		
Matches 46;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

QY 1 TCATATAAAATTATTTGCTTTCAGGAAAATTTTTCTGTATTAATAGATTCA 51
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 TCATATAAAATTATTTTACATCAGGAAAATTTTTCTGTATATTAGATTCA 51

RESULT 14
US-10-032-393-22

Query Match	84.3%	Score 43;	DB 14;	Length 94;
Best Local Similarity	90.2%;	Pred. No. 0.0037;		
Matches 46;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

```
QY      1 TCATAAAAAATTATTTGCTTCAGGAAATTTTTCGTATTAATAGATTCA 51
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      6 TCATAAAAAATTTATTTTACATCAGGAAATTTTTTCGTATATTAGATTCA 56
```

```

RESULT 15
US-10-032-393-23/c
; Sequence 23, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Wall, Daniel
; APPLICANT: Gross, Molly
; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
; FILE REFERENCE: ELITRA.010A
; CURRENT APPLICATION NUMBER: US/10/032,393
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/259,434
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/948,993
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Xyl-T5-DD complement

```

US-10-032-393-23				
Query Match	84.3%;	Score 43;	DB 14;	length 95;
Best Local Similarity	90.2%;	Pred. No. 0.0037;		
Matches 46;	Conservative	0;	Mismatches 5;	Indels 0;
				Gaps 0;

```

Oy      1 TCATAAAAAATTATTGCTTCAGGAAATTTTCTGTATATAGATTCA 51
          |||||
Db      93 TCATAAAAAATTTATTTCATCAGGAAATTTTCTGTATATTAGATTCA 43

```

Search completed: April 7, 2004, 05:42:40
Job time : 1006 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2004, 03:21:00 ; Search time 2008 Seconds

(without alignments)
758.452 Million cell updates/sec

Title: US-10-032-393-36

Perfect score: 51

Sequence: 1 tcataaaaaatttattgtct.....ttttctgtataatagattca 51

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30.2	59.2	318	14	CF350907 r156h06.y
2	29.4	57.6	358	9	AW049113 CF350907 r156h06.y
3	29.4	57.6	534	10	BB365884 AW049113 UI-M-BH1-
4	29.4	57.6	667	10	BB080413 BB365884 BB365884

5	29.4	57.6	768	13	BQ174160	BQ174160 UI-M-DJ2-
6	29.4	57.6	2505	11	AK048039	AK048039 Mus muscu
7	29.4	57.6	3403	11	AK034193	AK034193 Mus muscu
8	29.2	57.3	356	9	AI394884	AI394884 MA001291.
9	29.2	57.3	412	9	AA219512	AA219512 zq99g04.r
10	29	56.9	130	28	B2128980	B2128980 CH230-452
11	29	56.9	595	28	B2145989	B2145989 CH230-452
12	29	56.9	1048	28	B2184761	B2184761 CH230-423
13	28.8	56.5	560	28	B2194126	B2194126 CH230-465
14	28.8	56.5	654	28	B2216912	B2216912 CH230-417
15	28.8	56.5	773	14	CF406767	CF406767 CH3#044 C
16	28.8	56.5	875	28	B2192372	B2192372 CH230-465
17	28.4	55.7	412	29	AG242333	AG242333 lotus cor
18	28.2	55.3	140	28	AF056259	AF056259 AF056259
19	28.2	55.3	611	28	BH741163	BH741163 gt28b09.g
20	28.2	55.3	733	28	BH957079	BH957079 odj02a12.
21	28.2	55.3	757	28	BH992006	BH992006 oe11lc02.
22	28.2	55.3	834	13	BU746323	BU746323 CH3#003 D
23	28	54.9	659	14	CB431012	CB431012 606949 MA
24	28	54.9	729	14	CB4330297	CB4330297 606181 MA
25	27.8	54.5	381	10	AW522148	AW522148 UI-R-BOO-
26	27.8	54.5	748	28	BH670666	BH670666 BOMBC18TF
27	27.6	54.1	438	28	AQ782840	AQ782840 HS_5380_B
28	27.6	54.1	824	28	BH669814	BH669814 BOMAE23TF
29	27.4	53.7	571	28	BH506288	BH506288 BOGRV16TF
30	27.4	53.7	603	9	AA799484	AA799484 EST188981
31	27.4	53.7	641	28	BZ082391	BZ082391 1le41b09.
32	27.4	53.7	702	29	CE003137	CE003137 tigr-gss-
33	27.4	53.7	718	28	BH995398	BH995398 ceg92906.
34	27.4	53.7	760	28	BH605836	BH605836 BOGXW23TR
35	27.4	53.7	993	28	BH692567	BH692567 BOMJY76TR
36	27.4	53.7	1340	29	CG751618	CG751618 P046-1-D0
37	27.2	53.3	101	28	BZ217382	BZ217382 CH230-250
38	27.2	53.3	292	9	AA365198	AA365198 EST76173
39	27.2	53.3	357	28	BZ269137	BZ269137 CH230-375
40	27.2	53.3	378	28	BZ199225	BZ199225 CH230-495
41	27.2	53.3	450	29	CE706869	CE706869 tigr-gss-
42	27.2	53.3	544	28	BZ217207	BZ217207 CH230-372
43	27.2	53.3	546	28	BZ177519	BZ177519 CH230-493
44	27.2	53.3	560	28	BZ214923	BZ214923 CH230-466
45	27.2	53.3	631	28	BZ219091	BZ219091 CH230-259

ALIGNMENTS

RESULT 1
CF350907 318 bp mRNA linear EST 20-AUG-2003
LOCUS r156h06.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica
DEFINITION cDNA 5', mRNA sequence.
ACCESSION CF350907
VERSION CF350907.1 GI:33953420
KEYWORDS EST.
SOURCE Meloidogyne javanica (root-knot nematode)
ORGANISM Meloidogyne javanica
REFERENCE 1 (bases 1 to 318)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theisling,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
Tsagarelisvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)

TITLE JOURNAL
COMMENT The Washington Univ. Nematode EST Project, 1999
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Fax: 314 286 1810
Email: est@watson.wustl.edu
Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (DynaI) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractioned on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information.
Putative full length read
The vector to vector length is 319
Seq primer: Sp6.

FEATURES

source

Location/Qualifiers
1. 318
/organism="Meloidogyne javanica"
/mol_type="mRNA"
/db_xref="taxon:6303"
/tissue_type="whole organism"
/dev_stage="J2"
/lab_host="DH10B"
/clone_lib="Meloidogyne javanica J2 SMART pGEM"
/note="Vector: plasmid (ampicillin resistant); Site 1:
XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (DynaI) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractioned on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

ORIGIN

Query Match 59.2%; Score 30.2; DB 14; Length 318;
Best Local Similarity 81.4%; Pred. No. 2.9e+02;
Matches 35; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CATAAAAATTATTTGCTTCAGGAAATTTTCTGTATAT 44
80 CAAAAAGAAATTATTTATATCAGGGAATTTTCTGTATAT 122

RESULT 2
LOCUS AM049113 358 bp mRNA linear EST 18-SEP-1999
DEFINITION UI-M-BH1-amt-g-11-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone
UI-M-BH1-amt-g-11-0-UI 3', mRNA sequence.
ACCESSION AM049113
VERSION AM049113.1 GI:5909642
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 358)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704447
PUBMED 8889548
COMMENT Contact: Chin, H

National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag served to identify it as a clone from the normalized basal ganglia library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence:
15-92, >(TA)n#Simple-repeat
Seq primer: M13 Forward
POLYA=yes.

FEATURES

source

Location/Qualifiers
1. 358
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH1-amt-g-11-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH_BMAP_M_S2"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH_BMAP_M_S2 library is a subtracted library derived from NIH_BMAP_M_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.
TAG_TISSUE=basal-ganglia
TAG_LIB=NIH_BMAP_M_S2
TAG_SEQ=TGTAC"

ORIGIN

Query Match 57.6%; Score 29.4; DB 9; Length 358;
Best Local Similarity 76.6%; Pred. No. 4.5e+02;
Matches 36; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 ATAAAAAATTATTTGCTTCAGGAAATTTTCTGTATATAGATT 49
20 ATATATATTTATTTGCATACAGAAATATTTTCTATTTACATT 66

RESULT 3
LOCUS BB365884/c 534 bp mRNA linear EST 24-OCT-2001
DEFINITION BB365884 RIKEN full-length enriched, 16 days embryo head Mus musculus cDNA clone C130031F03 3', mRNA sequence.
ACCESSION BB365884
VERSION BB365884.2 GI:16406384
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 534)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,

Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jul 12, 2000 this sequence version replaced gi:9077712.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

FEATURES

source

1.534
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C130031F03"
/sex="mixed"
/tissue_type="head"
/dev_stage="16 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 16 days embryo
head"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGATTCTCGAGTTAATTAATTAATCCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I"

ORIGIN

Query Match 57.6%; Score 29.4; DB 10; Length 534;
Best Local Similarity 76.6%; Pred. No. 3.9e+02;
Matches 36; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 ATAAAAATTATTCCTTCAGGAAATTTTCTGTATATAGATT 49

Db 305 ATAAATATATTATTGCATACAGAAATATTATTTCTATTATACATT 259

RESULT 4
BB080413/c 667 bp mRNA linear EST 18-OCT-2001

LOCUS BB080413 RIKEN full-length enriched, adult male diencephalon Mus
DEFINITION musculus cDNA clone 9330162L04 3', mRNA sequence.

ACCESSION BB080413
VERSION BB080413.2 GI:16260594

KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 667)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)

TITLE On Jun 21, 2000 this sequence version replaced gi:8645473.
JOURNAL Contact: Yoshihide Hayashizaki
COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/

FEATURES

Location/Qualifiers

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

source

1..667

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="9330162L04"

/sex="male"

/tissue_type="diencephalon"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, adult male diencephalon"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCTCGAGTTAATTAATTAATCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

ORIGIN

Query Match 57.6%; Score 29.4; DB 10; Length 667;

Best Local Similarity 76.6%; Pred. No. 3.7e+02;

Matches 36; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 ATAAAAAATTATTGCTTTCAGGAAATTTTCTGTATATAGATT 49

|||||

Db 662 ATATATATTATTGCAATACAGAAATATTATTCTATTATACATT 616

RESULT 5

LOCUS BQ174160 768 bp mRNA linear EST 30-APR-2002

DEFINITION UI-M-DJ2-bvw-c-09-0-UI.s1 NIH_BMAP_DJ2 Mus musculus cDNA clone

UI-M-DJ2-bvw-c-09-0-UI 3', mRNA sequence.

BQ174160

accession

BQ174160

keywords

BQ174160.1 GI:20349651

EST.

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 768)

Ronaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene discovery

Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: MEST@mail.nih.gov

Tissue Procurement: Dr. Robin Davisson

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA sequence: 16-93, >(TA)n#simple_repeat

Seq primer: M13 FORWARD

POLYA=yes.

FEATURES

source

Location/Qualifiers

1..768

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="UI-M-DJ2-bvw-c-09-0-UI"

/tissue_type="subfornical organ and postrema"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="NIH_BMAP_DJ2"

/note="Organ: brain; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-M-DJ2 is a subtracted cDNA library constructed according to Ronaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is: GCTACATGAT, subfornical organ and area postrema.

TAG_TISSUE=subfornical organ and postrema

TAG_LIB=UI-M-DJ2

TAG_SEQ=GCTACATGAT"

ORIGIN

Query Match 57.6%; Score 29.4; DB 13; Length 768;

Best Local Similarity 76.6%; Pred. No. 3.5e+02;

Matches 36; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 ATAAAAAATTATTGCTTTCAGGAAATTTTCTGTATATAGATT 49

|||||

Db 21 ATATATATTATTGCAATACAGAAATATTATTCTATTATACATT 67

RESULT 6

LOCUS AK048039/c 2505 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30031F03 product:unknown EST, full insert sequence.

AK048039

accession

AK048039.1 GI:26092610

keywords

AK048039

keywords

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

2

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

3

Shibata,K., Itch,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itch,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE
JOURNAL
REFERENCE
AUTHORS
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE
JOURNAL
REFERENCE
AUTHORS
6
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2505)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE
JOURNAL
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES
source
1. .2505
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:C130031F03"
/db_xref="MGI:2414069"
/db_xref="taxon:10090"
/clone="C130031F03"
/issue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="16 days embryo"
1. .2505
/note="unknown EST (GB|BI735511, evidence: BLASTN, 99%, match=817)"
misc_feature
ORIGIN
Query Match 57.6%; Score 29.4; DB 11; Length 2505;
Best Local Similarity 76.6%; Pred. No. 2.3e+02;
Matches 36; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QX 3 ATAAAAATTTATTGCTTTCAGGAAATTTTCTGTATAATAGATT 49
|||||
Db 2274 ATAATATATTATTGCAATACAGAAATATTATTCTATTATACATT 2228

RESULT 7
AK034193/c
LOCUS
DEFINITION
AK034193 3403 bp mRNA linear HTC 18-SEP-2003
Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330162U04 product:unknown EST, full insert sequence.
ACCESSION
AK034193
VERSION
AK034193.1 GI:26083816
KEYWORDS
HTC, CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
1
Carninci,P. and Hayashizaki,Y.
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
2
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
3
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
4
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
5
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Taehiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
6
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
7
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE
JOURNAL
REFERENCE
AUTHORS
8
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
9
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE
JOURNAL
REFERENCE
AUTHORS
10
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3403)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE
JOURNAL
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,

Fax:81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>.

FEATURES
source
1..3403
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:9330162L04"
/db_xref="MGI:2358388"
/db_xref="taxon:10090"
/clone="9330162L04"
/sex="male"
/tissue_type="diencephalon"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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/note="unknown EST (GB|BI735511, evidence: BLASTN, 99%, match=817)"

ORIGIN

Query Match
Best Local Similarity 57.6%; Score 29.4; DB 11; Length 3403;
Matches 36; Conservativity 0; Mismatches 11; Indels 0; Gaps 0;

QY
3 ATAAAAAATTATTGCTTCAGGAAATTTTCTGTATATAGATT 49
|||||
3391 ATATATATATTATTGCATACAGAAATATTATTCTATATACATT 3345
|||||

Db
3391 ATATATATATTATTGCATACAGAAATATTATTCTATATACATT 3345
|||||

RESULT 8
AI394884 356 bp mRNA linear EST 04-FEB-1999
LOCUS MA001291.C8F Soares normalized S8W Schistosoma mansoni CDNA 3',
DEFINITION mRNA sequence.
ACCESSION AI394884 GI:4224431
VERSION AI394884.1 GI:4224431
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoida; Schistosomatidae; Schistosoma.
1 (bases 1 to 356)
Bailey,J.A., Bentley,K., Blanton,R.E., Soares,M.B. and Chakravarti,A.
Expressed sequence tags from a normalized adult Schistosoma mansoni library
Unpublished (1999)
Contact: Chakravarti A
Department of Genetics
Case Western Reserve University
2109 Adelbert Rd, Cleveland, OH 44106, USA
Tel: 216-368-5847
Fax: 216-368-5857
Email: axc39@po.cwru.edu
Additional data regarding this EST may be found at <http://genome.cwru.edu/schistosoma/est/S8west.html>
Seq primer: M13 Forward.

FEATURES
source
1..356
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/strain="Puerto Rican"
/db_xref="taxon:6183"
/sex="mixed"
/dev_stage="8 week old adult worms"
/lab_host="Mus musculus"

JOURNAL
COMMENT

/clone_lib="Soares normalized S8W"
/note=Vector: pT7T3-pac; Site_1: NotI; Site_2: EcoRI;
Note: normalization has resulted in an increased frequency of the rare contaminating mouse (host) sequences (~10%).
For details of library construction see: Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two Approaches to Facilitate Gene Discovery. 1996. Genome Research 6: 791-806"

ORIGIN

Query Match
Best Local Similarity 74.0%; Score 29.2; DB 9; Length 356;
Matches 37; Conservativity 0; Mismatches 13; Indels 0; Gaps 0;

QY
2 CATAAAAAATTATTGCTTCAGGAAATTTTCTGTATATAGATTCA 51
|||||
140 CATTAATAATCTAATCTTCTTAACAATAATCTTCTGTGAATAGATTAA 189
|||||

Db
140 CATTAATAATCTAATCTTCTTAACAATAATCTTCTGTGAATAGATTAA 189
|||||

RESULT 9
AA219512 412 bp mRNA linear EST 07-FEB-1997
LOCUS zq99g04.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens
DEFINITION CDNA clone IMAGE:650166 5', mRNA sequence.
ACCESSION AA219512
VERSION AA219512.1 GI:1833571
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 412)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaekis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

JOURNAL
MEDLINE
PUBMED
8889549
TITLE
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINT; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 262.

FEATURES
source
1..412
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5276755"
/db_xref="taxon:9606"
/clone="IMAGE:650166"
/tissue_type="neuroepithelial cells"
/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene NT2 neuronal precursor 937230"
/note="Organ: brain; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Uninduced, exponentially growing neuroepithelial cells (Ntera-2/cl.D1). Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGAG 3', ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

ORIGIN

Query Match
57.3%; Score 29.2; DB 9; Length 412;

Best Local Similarity 72.5%; Pred. No. 4.8e+02;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Dy 1 TCATAAAAAATTATTTGCTTTCAGGAAAATTTTCTGTATTAATGATTTCA 51
| | | | | | | | | | | | | | | | | |
Db 122 TCTNTAAAGAATGATTTTTCTTTCTTAAAAATTTCTGTGTATTCTTAAATTTA 722

RESULT 10	BZ128980	LOCUS	BZ128980	130 bp	DNA	linear	GSS 11-OCT-2002
DEFINITION	CH230-452M22.TJ CHORI-230 Segment 2						Rattus norvegicus genomic clone
	CH230-452M22, genomic survey sequence.						

ACCESSION	BZ128580	
VERSION	BZ128980.1	GI:23769927
KEYWORDS	GSS.	
SOURCE	Rattus norvegicus	(Norway rat)
ORGANISM	Rattus norvegicus	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 130)	Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Riggs, F., de Jong, P. and Fraser, C.M.	Rat BAC End Sequences from Library CHORI-230	Mbol segment	Unpublished (1999) Contact: Shaying Zhao

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 452 row: N column: 22
Seq primer: SP6
Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .130

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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNhsd/MCW"
/db_xref="taxon:10116"
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/sex="Female"
/cell_type="Brain"
/clone_1ib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI;
CHORI-230 Rat (BN/SsNhsd/MCW) BAC library produced by
Pieter de Jong"

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ORIGIN
Query Match      56.9%; Score 29; DB 28; Length 130;
Best Local Similarity 86.5%; Pred. No. 8e+02;
Matches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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OY 5 AAAAAATTATTTGCTTTCAGGAAAATTTTCTGTAT 41
 |||||
Db 10 AAAAATTTGATTCATTCATGAATAATTTTCTGTAT 46
 |||||

RESULT 11	
BZ145989	
LOCUS	
DEFINITION	BZ145989 595 bp DNA linear GSS 11-OCT-2002
ACCESSION	CH230-452N22.TU CHORI-230 Segment 2 Rattus norvegicus genomic clone
	CH230-452N22, genomic survey sequence.
	BZ145989

VERSION	B2145989.1	GI:23786936
KEYWORDS	GSS.	
SOURCE	Rattus norvegicus (Norway rat)	
ORGANISM	Rattus norvegicus	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 595)	Shao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Riggs,F., de Jong,P. and Fraser,C.M.	Rat BAC End sequences from library CHORI-230	Mbol segment	Unpublished (1999)
		Other_GSSs:	CH230-452N22.TV	

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.chi.org).
Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/> or http://www.chori.org/tdb/bac_ends/rat/bac_end_intro.html)
Page: 452 row: N column: 22
Seq primer: SP6
Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .595

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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SSNhsd/MCw"
/db_xref="taxon:10116"
/clone="CH230-452N22"
/sex="Female"
/cell_type="Brain"
/clone_1ib="CHORI-230 Segment 2"
/note="vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
CHORI-230 Rat (BN/SSNhsd/MCw) BAC library produced by
Pieter de Jong"

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Query Match	56.9%	Score 29;	DB 28;	Length 595;
Best Local Similarity	86.5%;	Pred. No. 4.8e+02;		
Matches 32;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

QY 5 AAAAAATTATTGCTTCAGGAAAAATTTTCGTAT 41
| | | | | | | | | | | | | | | | | | | | | |
Db 485 AAAAAATTGATGTCATTCATGAAAAATTTTCTGTAT 521

RESULT 12	
BZ184761/c	
LOCUS	BZ184761
DEFINITION	CH230-423F16.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
	CH230-423F16, genomic survey sequence.

ACCESSION	BZ184761	
VERSION	BZ184761.1	GI:23834700
KEYWORDS	GSS.	
SOURCE	Rattus norvegicus	(Norway rat)
ORGANISM	Rattus norvegicus	

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 1048)	Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.	Rat BAC End Sequences from Library CHOR1-230 MboI segment	unpublished (1999)

COMMENT
Other GSSs: CH230-423F16.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 423 row: F column: 16
Seq primer: SP6
Class: BAC ends.

FEATURES
source
1. 1048
/location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-423F16"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN
Query Match 56.9%; Score 29; DB 28; Length 1048;
Best Local Similarity 86.5%; Pred. No. 4e+02;
Matches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 AAAAAATTATTGCTTTCAGAAAAATTTCTGTAT 41
|||||
108 AAAAAATTGATTGATTCATTCATGAAAAATTTCTGTAT 72
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RESULT 13
B2194126 560 bp DNA linear GSS 11-OCT-2002
LOCUS
DEFINITION CH230-465D15.TVB CHORI-230 Segment 2 Rattus norvegicus genomic
clone CH230-465D15, genomic survey sequence.
ACCESSION B2194126
VERSION B2194126.1 GI:23852178
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 560)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-465D15.TVB
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering_information.htm). BAC end

TITLE
JOURNAL
COMMENT

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 465 row: D column: 15
Seq primer: SP6
Class: BAC ends.

FEATURES
source
1. 560
/location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-465D15"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN
Query Match 56.5%; Score 28.8; DB 28; Length 560;
Best Local Similarity 82.5%; Pred. No. 5.5e+02;
Matches 33; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 CATAAAAATTATTGCTTTCAGAAAAATTTCTGTAT 41
|||||
526 CTTAGAAATTTAATTCATTCATGAAAAATTTCTGTAT 487
|||||

RESULT 14
B2216912 654 bp DNA linear GSS 11-OCT-2002
LOCUS
DEFINITION CH230-41703.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-41703, genomic survey sequence.
ACCESSION B2216912
VERSION B2216912.1 GI:23875270
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 654)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-41703.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 417 row: O column: 3
Seq primer: SP6
Class: BAC ends.

FEATURES
source
1. 654
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-41703"
/sex="Female"
/cell_type="Brain"

TITLE
JOURNAL
COMMENT

Job time : 2013 secs

/clone_lib="CHORI-230 Segment 2"
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SSNhsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN

Query Match 56.5%; Score 28.8; DB 28; Length 654;
Best Local Similarity 82.5%; Pred. No. 5.2e+02;
Matches 33; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 CATAAAAAATTATTTGCTTCAGGAAATTTTCTGTAT 41
Db 513 CTTAGAAATTTTATTCATTCATGAAATTTTCTGTAT 474

RESULT 15

CF406767/c

LOCUS

DEFINITION

CF406767 773 bp mRNA linear EST 02-SEP-2003
CH3#044_C08T3 Canine heart normalized cDNA library in pBluescript

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 773)
Yl.Y., Desai,R., Olarte,M., Henthorn,P. and George A.L.
Expressed sequence tags from Canine heart
Unpublished (2003)
Other ESTs: CH3#044_C08T7
COMMENT
Contact: George AL
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661
Email: al.george@vanderbilt.edu
Insert Length: 1448 Std Error: 0.00
Seq primer: T3: ATTAACCTCCTACTAAAGGGA
High quality sequence start: 64
High quality sequence stop: 733.
Location/Qualifiers
1..773

FEATURES
Source
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CH3#044_C08"
/tissue_type="heart"
/cell_type="heart"
/dev_stage="mixed developmental stages (adult, 30 day - 40
day fetal)"
/clone_lib="Canine heart normalized cDNA library in
pBluescript"
/note="Organ: heart; Vector: pBluescript; Site 1: 5' of
vector NotI; Site 2: 3' of vector EcoRI; Tissue source:
dog heart (adult, 30 day - 40 day fetal), right and left
atria and ventricle. Dog breed - mixed (beagle, German
shepherd, pointer, Irish setter). Library construction:
oligo-dt primed"

ORIGIN

Query Match 56.5%; Score 28.8; DB 14; Length 773;
Best Local Similarity 75.0%; Pred. No. 4.9e+02;
Matches 36; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 CATAAAAAATTATTTGCTTCAGGAAATTTTCTGTATAATAGATT 49
Db 238 CTTAAAAAATTTTATGTATAGATAATAATTTTCTATATGATAGACT 191